

GenCore version 5.1.6  
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OM protein - protein search, using sw model.

Run on: July 28, 2003, 17:04:20 ; Search time 13 Seconds  
(without alignments)  
3.159 Million cell updates/sec

Title: US-09-930-125-3  
Perfect score: 54  
Sequence: 1 EEVLVPOQGF 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 41799 seqs, 4106219 residues

Total number of hits satisfying chosen parameters: 41799

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_AA\_New.\*  
1: /cgn2\_6/ptodata/2/paa/PCT\_NEW\_COMB.pcp.\*  
2: /cgn2\_6/ptodata/2/paa/US06\_NEW\_COMB.pcp.\*  
3: /cgn2\_6/ptodata/2/paa/US07\_NEW\_COMB.pcp.\*  
4: /cgn2\_6/ptodata/2/paa/US08\_NEW\_COMB.pcp.\*  
5: /cgn2\_6/ptodata/2/paa/US09\_NEW\_COMB.pcp.\*  
6: /cgn2\_6/ptodata/2/paa/US10\_NEW\_COMB.pcp.\*  
7: /cgn2\_6/ptodata/2/paa/US60\_NEW\_COMB.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	1255	1 PCT-US03-20322-213	Sequence 213, App
2	35	64.8	453	6 US-10-273-573-7709	Sequence 7709, App
3	35	64.8	474	6 US-10-273-573-9017	Sequence 9017, App
4	33	61.1	1224	1 PCT-US02-41730-2	Sequence 2, Appli
5	32	59.3	180	6 US-10-294-433-421	Sequence 421, App
6	31	57.4	245	6 US-10-273-573-6289	Sequence 6289, App
7	31	57.4	532	6 US-10-294-433-388	Sequence 388, App
8	31	57.4	1261	6 US-10-273-573-7512	Sequence 7512, App
9	31	57.4	2662	6 US-10-273-573-8548	Sequence 8548, App
10	31	57.4	2703	6 US-10-273-573-8538	Sequence 8538, App
11	31	57.4	2719	6 US-10-273-573-8996	Sequence 8996, App
12	31	57.4	2986	6 US-10-273-573-8550	Sequence 8550, App
13	31	57.4	3114	6 US-10-273-573-8546	Sequence 8546, App
14	31	57.4	3509	6 US-10-273-573-8544	Sequence 8544, App
15	31	57.4	4766	6 US-10-273-573-8539	Sequence 8539, App
16	31	57.4	4367	6 US-10-273-573-8549	Sequence 8549, App
17	31	57.4	5367	6 US-10-273-573-8547	Sequence 8547, App
18	30	55.6	221	6 US-10-273-573-6685	Sequence 6685, App
19	30	55.6	547	7 US-60-478-196-3018	Sequence 3018, App
20	30	55.6	670	7 US-60-478-196-3311	Sequence 3311, App
21	29	53.7	207	1 PCT-US03-20041-105	Sequence 105, App
22	29	53.7	257	6 US-10-273-573-5844	Sequence 5844, App
23	29	53.7	303	6 US-10-273-573-5845	Sequence 5845, App
24	29	53.7	349	1 PCT-US03-20041-80	Sequence 80, Appl
25	29	53.7	351	1 PCT-US03-20041-82	Sequence 82, Appl
26	29	53.7	351	1 PCT-US03-20041-91	Sequence 91, Appl

ALIGNMENTS

RESULT 1  
PCT-US03-20322-213  
; Sequence 213, Application PC/YUS0320322  
; GENERAL INFORMATION:  
; APPLICANT: Dana-Farber Cancer Institute, Inc., et al.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING  
; FILE REFERENCE: DPN-043PC  
; CURRENT APPLICATION NUMBER: PCT/US03/20322  
; PRIOR FILING DATE: 2003-06-27  
; PRIOR FILING DATE: 2002-06-27  
; NUMBER OF SEQ ID NOS: 340  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 213  
; LENGTH: 1255  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
PCT-US03-20322-213

Query Match 100.0%; Score 54; DB 1; Length 1255;  
Best Local Similarity 100.0%; Pred. No. 0.0064;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEVLVPOQGF 10  
Db 1021 EEVLVPOQGF 1030

RESULT 2  
US-10-273-573-7709  
; Sequence 7709, Application US/10273573  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc  
; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 21272-066 US/10/273,573  
; CURRENT APPLICATION NUMBER: US/10/273,573  
; PRIOR FILING DATE: 2002-10-18  
; PRIOR FILING DATE: 2000-04-18  
; PRIOR FILING DATE: 2000-04-18  
; PRIOR FILING DATE: 2001-01-26  
; NUMBER OF SEQ ID NOS: 10994  
; SOFTWARE: Custom  
; SEQ ID NO 7709  
; LENGTH: 453  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:

Sequence 110, App  
Sequence 99, Appl  
Sequence 6, Appli  
Sequence 5843, Ap  
Sequence 7295, Ap  
Sequence 11, Appl  
Sequence 13, Appl  
Sequence 12, Appl  
Sequence 14, Appl  
Sequence 10219, A  
Sequence 4, Appli  
Sequence 6, Appli  
Sequence 7, Appli  
Sequence 5, Appli  
Sequence 18, Appl  
Sequence 36, Appl  
Sequence 45, Appl  
Sequence 9500, Ap  
Sequence 8835, Ap

NAME/KEY: DOMAIN  
LOCATION: (168)...(183)  
OTHER INFORMATION: G-PROTEIN BETA WD-40 REPEAT SIGNATURE domain identified by  
OTHER INFORMATION: eMATRIX, accession number PR00320A, p-value=1.000e-10, raw score  
OTHER INFORMATION: 16.74  
FEATURE:  
NAME/KEY: DOMAIN  
LOCATION: (96)...(181)  
OTHER INFORMATION: WD domain, G-beta repeat domain identified by Pfam, accession  
OTHER INFORMATION: name WD40, E-value=1.1e-05, Pfam score of 32.3  
US-10-273-573-7709

Query Match 64.8%; Score 35; DB 6; Length 453;  
Best Local Similarity 50.0%; Pred. No. 9.1;  
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEYLVPOQGF 10  
:|:|:|:|:  
DB 300 DEHLIPOLGY 309

## RESULT 3

US-10-273-573-9017  
Sequence 9017, Application US/10273573  
GENERAL INFORMATION:  
APPLICANT: Hyseq, Inc  
TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES  
FILE REFERENCE: 21272-066  
CURRENT APPLICATION NUMBER: US/10/273,573  
CURRENT FILING DATE: 2002-10-18  
PRIOR APPLICATION NUMBER: 09/522,929  
PRIOR FILING DATE: 2000-04-18  
PRIOR APPLICATION NUMBER: 09/770,160  
PRIOR FILING DATE: 2001-01-26  
NUMBER OF SEQ ID NOS: 10994  
SOFTWARE: Custom  
SEQ ID NO 9017  
LENGTH: 474  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: DOMAIN  
LOCATION: (189)...(204)  
OTHER INFORMATION: G-PROTEIN BETA WD-40 REPEAT SIGNATURE domain identified by  
OTHER INFORMATION: eMATRIX, accession number PR00320A, p-value=1.000e-10, raw score  
OTHER INFORMATION: 16.74  
FEATURE:  
NAME/KEY: DOMAIN  
LOCATION: (117)...(202)  
OTHER INFORMATION: WD domain, G-beta repeat domain identified by Pfam, accession  
OTHER INFORMATION: name WD40, E-value=1.1e-05, Pfam score of 32.3  
US-10-273-573-9017

Query Match 64.8%; Score 35; DB 6; Length 474;  
Best Local Similarity 50.0%; Pred. No. 9.5;  
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEYLVPOQGF 10  
:|:|:|:|:  
DB 321 DEHLIPOLGY 330

## RESULT 4

PCT-US02-41730-2  
Sequence 2, Application PC/TUS0241730  
GENERAL INFORMATION:  
APPLICANT: Wyeth  
TITLE OF INVENTION: AGGREGANASE MOLECULES  
FILE REFERENCE: AM100884 PCT  
CURRENT APPLICATION NUMBER: PCT/US02/41730  
CURRENT FILING DATE: 2002-12-30  
PRIOR APPLICATION NUMBER: 60/344,895  
PRIOR FILING DATE: 2001-12-31

NUMBER OF SEQ ID NOS: 18  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 2  
LENGTH: 1224  
TYPE: PRT  
ORGANISM: Homo sapiens  
PCT-US02-41730-2

Query Match 61.1%; Score 33; DB 1; Length 1224;  
Best Local Similarity 85.7%; Pred. No. 62;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 YLVPQOG 9  
|:|:|:|:  
DB 1198 YLVPQHG 1204

## RESULT 5

US-10-294-433-421  
Sequence 421, Application US/10294433  
GENERAL INFORMATION:  
APPLICANT: Hyseq, Inc  
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
FILE REFERENCE: 792CIP4  
CURRENT APPLICATION NUMBER: US/10/294,433  
CURRENT FILING DATE: 2002-11-13  
PRIOR APPLICATION NUMBER: PCT/US01/14826  
PRIOR FILING DATE: 2001-05-16  
PRIOR APPLICATION NUMBER: 09/989,600  
PRIOR FILING DATE: 2001-11-21  
PRIOR APPLICATION NUMBER: 09/577,408  
PRIOR FILING DATE: 2000-05-18  
PRIOR APPLICATION NUMBER: 10/115,831  
PRIOR FILING DATE: 2002-04-02  
PRIOR APPLICATION NUMBER: 09/677,298  
PRIOR FILING DATE: 2000-09-22  
PRIOR APPLICATION NUMBER: 09/695,781  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: 10/150,802  
PRIOR FILING DATE: 2002-05-15  
PRIOR APPLICATION NUMBER: 09/715,869  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 10/167,379  
PRIOR FILING DATE: 2002-06-10  
PRIOR APPLICATION NUMBER: 09/775,330  
PRIOR FILING DATE: 2001-02-01  
NUMBER OF SEQ ID NOS: 864  
SOFTWARE: Custom  
SEQ ID NO 421  
LENGTH: 180  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-294-433-421

Query Match 59.3%; Score 32; DB 6; Length 180;  
Best Local Similarity 66.7%; Pred. No. 13;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EEYLVPOQOG 9  
|:|:|:|:  
DB 60 EEWLAPVQG 68

## RESULT 6

US-10-273-573-6289  
Sequence 6289, Application US/10273573  
GENERAL INFORMATION:  
APPLICANT: Hyseq, Inc  
TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES  
FILE REFERENCE: 21272-066  
CURRENT APPLICATION NUMBER: US/10/273,573  
CURRENT FILING DATE: 2002-10-18  
PRIOR APPLICATION NUMBER: 09/522,929

; PRIOR FILING DATE: 2000-04-18  
; PRIOR APPLICATION NUMBER: 09/770,160  
; PRIOR FILING DATE: 2001-01-26  
; NUMBER OF SEQ ID NOS: 10994  
; SOFTWARE: Custom  
; SEQ ID NO 6289  
; LENGTH: 245  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(245)  
; OTHER INFORMATION: Xaa = X or \* as defined in Table 2  
US-10-273-573-6289

Query Match 57.4%; Score 31; DB 6; Length 245;  
Best Local Similarity 55.6%; Pred. No. 27;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EYLVPOQG 9  
| | | : | : |  
Db 196 EYQIPEVG 204

## RESULT 7

US-10-294-433-388  
; Sequence 388, Application US/10294433  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc  
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 792CIP4  
; CURRENT APPLICATION NUMBER: US/10/294,433  
; CURRENT FILING DATE: 2002-11-13  
; PRIOR APPLICATION NUMBER: PCT/US01/14826  
; PRIOR FILING DATE: 2001-05-16  
; PRIOR APPLICATION NUMBER: 09/989,600  
; PRIOR FILING DATE: 2001-11-21  
; PRIOR APPLICATION NUMBER: 09/577,408  
; PRIOR FILING DATE: 2000-05-18  
; PRIOR APPLICATION NUMBER: 10/115,831  
; PRIOR FILING DATE: 2002-04-02  
; PRIOR APPLICATION NUMBER: 09/677,298  
; PRIOR FILING DATE: 2000-09-22  
; PRIOR APPLICATION NUMBER: 09/695,781  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: 10/150,802  
; PRIOR FILING DATE: 2002-05-15  
; PRIOR APPLICATION NUMBER: 09/715,869  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 10/167,379  
; PRIOR FILING DATE: 2002-06-10  
; PRIOR APPLICATION NUMBER: 09/775,330  
; PRIOR FILING DATE: 2001-02-01  
; NUMBER OF SEQ ID NOS: 864  
; SOFTWARE: Custom  
; SEQ ID NO 388  
; LENGTH: 532  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-294-433-388

Query Match 57.4%; Score 31; DB 6; Length 532;  
Best Local Similarity 55.6%; Pred. No. 62;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EYLVPOQG 9  
| | | : | : |  
Db 505 EYLIENAG 513

## RESULT 8

US-10-273-573-7512  
; Sequence 7512, Application US/10273573

; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc  
; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 21272-066  
; CURRENT APPLICATION NUMBER: US/10/273,573  
; CURRENT FILING DATE: 2002-10-18  
; PRIOR APPLICATION NUMBER: 09/522,929  
; PRIOR FILING DATE: 2000-04-18  
; PRIOR APPLICATION NUMBER: 09/770,160  
; PRIOR FILING DATE: 2001-01-26  
; NUMBER OF SEQ ID NOS: 10994  
; SOFTWARE: Custom  
; SEQ ID NO 7512  
; LENGTH: 1261  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-273-573-7512

Query Match 57.4%; Score 31; DB 6; Length 1261;  
Best Local Similarity 71.4%; Pred. No. 1.5e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LVPOQGF 10  
| | | : | : |  
Db 435 LLPQGF 441

## RESULT 9

US-10-273-573-8548  
; Sequence 8548, Application US/10273573  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc  
; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 21272-066  
; CURRENT APPLICATION NUMBER: US/10/273,573  
; CURRENT FILING DATE: 2002-10-18  
; PRIOR APPLICATION NUMBER: 09/522,929  
; PRIOR FILING DATE: 2000-04-18  
; PRIOR APPLICATION NUMBER: 09/770,160  
; PRIOR FILING DATE: 2001-01-26  
; NUMBER OF SEQ ID NOS: 10994  
; SOFTWARE: Custom  
; SEQ ID NO 8548  
; LENGTH: 2662  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; NAME/KEY: DOMAIN  
; LOCATION: (1002)...(2138)  
; OTHER INFORMATION: BRCA2 repeat domain identified by Pfam, accession name  
; OTHER INFORMATION: BRCA2\_repeat, E-value=2e-111, Pfam score of 383.6  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(2662)  
; OTHER INFORMATION: Xaa = X or \* as defined in Table 2  
US-10-273-573-8548

Query Match 57.4%; Score 31; DB 6; Length 2662;  
Best Local Similarity 55.6%; Pred. No. 3.4e+02;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 EYLVPOQGF 10  
| | | : | : |  
Db 2089 EHLISQGF 2097

## RESULT 10

US-10-273-573-8538  
; Sequence 8538, Application US/10273573  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc  
; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 21272-066

; CURRENT APPLICATION NUMBER: US/10/273,573

; CURRENT FILING DATE: 2002-10-18

; PRIOR APPLICATION NUMBER: 09/522,929

; PRIOR FILING DATE: 2000-04-18

; PRIOR APPLICATION NUMBER: 09/770,160

; PRIOR FILING DATE: 2001-01-26

; NUMBER OF SEQ ID NOS: 10994

; SOFTWARE: Custom

; SEQ ID NO 8538

; LENGTH: 2703

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: DOMAIN

; LOCATION: (1026)..(1064)

; OTHER INFORMATION: S-adenosyl-L-homocysteine hydrolase proteins domain

; OTHER INFORMATION: identified by eMATRIX, accession number BL00738C, p-value=9.357e-

; OTHER INFORMATION: 09, raw score of 16.53

; FEATURE:

; NAME/KEY: DOMAIN

; LOCATION: (3)..(2576)

; OTHER INFORMATION: BRCA2 repeat domain identified by Pfam, accession name

; OTHER INFORMATION: BRCA2\_repeat, E-value=3.2e-106, Pfam score of 366.3

US-10-273-573-8538

Query Match 57.4%; Score 31; DB 6; Length 2703;

Best Local Similarity 55.6%; Pred. No. 3.4e+02;

Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 EYLVPQOGF 10

I::I::I::I

Db 365 EHLISQKGF 373

RESULT 11

US-10-273-573-8996

; Sequence 8996, Application US/10273573

; GENERAL INFORMATION:

; APPLICANT: Hyseq, Inc

; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES

; FILE REFERENCE: 21272-066

; CURRENT APPLICATION NUMBER: US/10/273,573

; CURRENT FILING DATE: 2002-10-18

; PRIOR APPLICATION NUMBER: 09/522,929

; PRIOR FILING DATE: 2000-04-18

; PRIOR APPLICATION NUMBER: 09/770,160

; PRIOR FILING DATE: 2001-01-26

; NUMBER OF SEQ ID NOS: 10994

; SOFTWARE: Custom

; SEQ ID NO 8996

; LENGTH: 2719

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: DOMAIN

; LOCATION: (2481)..(2526)

; OTHER INFORMATION: Amino acid permeases proteins domain identified by eMATRIX,

; OTHER INFORMATION: accession number BL00218D, p-value=8.043e-37, raw score of 21.49

; FEATURE:

; NAME/KEY: DOMAIN

; LOCATION: (1215)..(1561)

; OTHER INFORMATION: Cell cycle protein domain identified by Pfam, accession name

; OTHER INFORMATION: FTSW\_RODA\_SPOVE, E-value=1e-80, Pfam score of 281.6

US-10-273-573-8996

Query Match 57.4%; Score 31; DB 6; Length 2719;

Best Local Similarity 62.5%; Pred. No. 3.4e+02;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 YLVPQOGF 10

I::I::I::I

Db 2621 YLLPQKAF 2628

RESULT 12

US-10-273-573-8550

; Sequence 8550, Application US/10273573

; GENERAL INFORMATION:

; APPLICANT: Hyseq, Inc

; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES

; FILE REFERENCE: 21272-066

; CURRENT APPLICATION NUMBER: US/10/273,573

; CURRENT FILING DATE: 2002-10-18

; PRIOR APPLICATION NUMBER: 09/522,929

; PRIOR FILING DATE: 2000-04-18

; PRIOR APPLICATION NUMBER: 09/770,160

; PRIOR FILING DATE: 2001-01-26

; NUMBER OF SEQ ID NOS: 10994

; SOFTWARE: Custom

; SEQ ID NO 8550

; LENGTH: 2986

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: DOMAIN

; LOCATION: (2946)..(2984)

; OTHER INFORMATION: S-adenosyl-L-homocysteine hydrolase proteins domain

; OTHER INFORMATION: identified by eMATRIX, accession number BL00738C, p-value=9.

; OTHER INFORMATION: 09, raw score of 16.53

; FEATURE:

; NAME/KEY: DOMAIN

; LOCATION: (92)..(2335)

; OTHER INFORMATION: BRCA2 repeat domain identified by Pfam, accession name

; OTHER INFORMATION: BRCA2\_repeat, E-value=6.2e-162, Pfam score of 551.4

; FEATURE:

; NAME/KEY: misc\_feature

; LOCATION: (1)..(2986)

; OTHER INFORMATION: xaa = x or \* as defined in Table 2

US-10-273-573-8550

Query Match 57.4%; Score 31; DB 6; Length 2986;

Best Local Similarity 55.6%; Pred. No. 3.8e+02;

Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 EYLVPQOGF 10

I::I::I::I

Db 2286 EHLISQKGF 2294

RESULT 13

US-10-273-573-8546

; Sequence 8546, Application US/10273573

; GENERAL INFORMATION:

; APPLICANT: Hyseq, Inc

; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES

; FILE REFERENCE: 21272-066

; CURRENT APPLICATION NUMBER: US/10/273,573

; CURRENT FILING DATE: 2002-10-18

; PRIOR APPLICATION NUMBER: 09/522,929

; PRIOR FILING DATE: 2000-04-18

; PRIOR APPLICATION NUMBER: 09/770,160

; PRIOR FILING DATE: 2001-01-26

; NUMBER OF SEQ ID NOS: 10994

; SOFTWARE: Custom

; SEQ ID NO 8546

; LENGTH: 3114

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: DOMAIN

; LOCATION: (2551)..(2589)

; OTHER INFORMATION: S-adenosyl-L-homocysteine hydrolase proteins domain

; OTHER INFORMATION: identified by eMATRIX, accession number BL00738C, p-value=9.

; OTHER INFORMATION: 09, raw score of 16.53

; FEATURE:

; NAME/KEY: DOMAIN

```
; LOCATION: (1002)..(1938)
; OTHER INFORMATION: BRCA2 repeat domain identified by Pfam, accession name
; OTHER INFORMATION: BRCA2_repeat, E-value=9.6e-108, Pfam score of 371.4
US-10-273-573-8546
```

```
Query Match      57.4%; Score 31; DB 6; Length 3114;
Best Local Similarity 55.6%; Pred. No. 4e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 EYLVPOQGF 10
      |:|: |:|
Db      1890 EHLISQKGF 1898
```

## RESULT 14

```
US-10-273-573-8544
; Sequence 8544, Application US/10273573
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-066
; CURRENT APPLICATION NUMBER: US/10/273,573
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 09/522,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: 09/770,160
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 10994
; SOFTWARE: Custom
; SEQ ID NO 8544
; LENGTH: 3509
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (716)..(3025)
; OTHER INFORMATION: BRCA2 repeat domain identified by Pfam, accession name
; OTHER INFORMATION: BRCA2_repeat, E-value=1.8e-192, Pfam score of 652.8
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(3509)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-273-573-8544
```

```
Query Match      57.4%; Score 31; DB 6; Length 3509;
Best Local Similarity 55.6%; Pred. No. 4.5e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 EYLVPOQGF 10
      |:|: |:|
Db      2977 EHLISQKGF 2985
```

## RESULT 15

```
US-10-273-573-8539
; Sequence 8539, Application US/10273573
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-066
; CURRENT APPLICATION NUMBER: US/10/273,573
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 09/522,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: 09/770,160
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 10994
; SOFTWARE: Custom
; SEQ ID NO 8539
; LENGTH: 4766
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
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```
; NAME/KEY: DOMAIN
; LOCATION: (1732)..(1770)
; OTHER INFORMATION: S-adenosyl-L-homocysteine hydrolase proteins domain
; OTHER INFORMATION: identified by eMATRIX, accession number BL00738C, p-value=9.35
; OTHER INFORMATION: 09, raw score of 16.53
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (694)..(3434)
; OTHER INFORMATION: BRCA2 repeat domain identified by Pfam, accession name
; OTHER INFORMATION: BRCA2_repeat, E-value=3.1e-166, Pfam score of 565.7
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(4766)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-273-573-8539
```

```
Query Match      57.4%; Score 31; DB 6; Length 4766;
Best Local Similarity 55.6%; Pred. No. 6.2e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
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```
QY      2 EYLVPOQGF 10
      |:|: |:|
Db      1071 EHLISQKGF 1079
```

```
Search completed: July 28, 2003, 17:14:00
Job time : 13 secs
```

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 28, 2003, 16:45:39 ; Search time 22 Seconds  
(without alignments)  
21.376 Million cell updates/sec

Title: US-09-930-125-3  
Perfect score: 54  
Sequence: 1 EEVLVPQGF 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match, 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54	100.0	245	1 ERB2_MOUSE	P70424 mus musculus
2	54	100.0	1254	1 ERB2_MESAU	O60553 mesocricetu
3	54	100.0	1255	1 ERB2_HUMAN	P04626 homo sapien
4	54	100.0	1257	1 ERB2_RAT	P08494 rattus norv
5	50	92.6	1210	1 EGFR_HUMAN	P00533 homo sapien
6	50	92.6	1210	1 EGFR_MOUSE	Q01279 mus musculus
7	46	85.2	540	1 ERBB_AVIEU	P11273 avian eryth
8	46	85.2	604	1 ERBB_AVIER	P00535 avian eryth
9	46	85.2	634	1 ERBB_ALV	P00534 avian leuko
10	38	70.4	232	1 YH73_SYNY3	P73623 synecocyst
11	37	68.5	95	1 ERB4_MOUSE	P51176 bos taurus
12	37	68.5	687	1 TGM2_BOVIN	P51176 bos taurus
13	37	68.5	687	1 TGM2_HUMAN	P21980 homo sapien
14	37	68.5	689	1 TGM2_CAVCU	P08587 cavia cutie
15	37	68.5	1308	1 ERB4_HUMAN	Q15303 homo sapien
16	37	68.5	1308	1 ERB4_RAT	Q62956 rattus norv
17	36	66.7	541	1 FTCD_HUMAN	O95954 h formimido
18	35	64.8	391	1 CAJ1_YEAST	P39101 saccharomyc
19	35	64.8	686	1 TGM2_MOUSE	P21981 mus musculus
20	35	64.8	917	1 NTA2_ARATH	P1035 arabidopsis
21	35	64.8	1242	1 MSH6_YEAST	Q03834 saccharomyc
22	35	64.8	2269	1 WRG9_HUMAN	Q9usi6 homo sapien
23	34	63.0	262	1 YF59_HELPJ	Q82190 helicobacte
24	34	63.0	364	1 MURG_THETN	Q82196 thermoaer
25	34	63.0	365	1 MURG_SHEVI	Q9fin0 shewanella
26	34	63.0	474	1 SYE_BUCAP	Q8ka47 buchnera ap
27	34	63.0	541	1 FTCD_PIG	P53603 s formimido
28	34	63.0	598	1 N5M5_PETWA	Q35543 petromyzon
29	34	63.0	988	1 TNP2_ECOLI	P06694 escherichia
30	34	63.0	997	1 Y414_MYCPN	P75183 mycoplasma
31	34	63.0	1097	1 TOLL_DROME	P08953 drosophila
32	34	63.0	2290	1 POLG_MOUSE	P03304 encephalomy
33	34	63.0	2292	1 POLG_EMCVB	P17593 encephalomy

34	34	63.0	2292	1 POLG_EMCVD	P17594 encephalomy
35	33	61.1	262	1 YF59_HELPY	P55986 helicobacte
36	33	61.1	370	1 MYOM_APLCA	P15513 a myomoduli
37	33	61.1	390	1 NCF1_MOUSE	Q09014 mus musculu
38	33	61.1	392	1 YAV1_SCHPO	Q10209 schizosacch
39	33	61.1	439	1 LIP1_DROME	O46107 drosophila
40	33	61.1	459	1 T7L2_MOUSE	Q92480 mus musculu
41	33	61.1	541	1 FTCD_MOUSE	O91x04 m formimido
42	33	61.1	541	1 FTCD_RAT	O88618 r formimido
43	33	61.1	584	1 T7L1_MOUSE	O921j1 mus musculu
44	33	61.1	588	1 T7L1_HUMAN	O9hcs4 homo sapien
45	33	61.1	619	1 T7L2_HUMAN	O9nqb0 homo sapien

#### ALIGNMENTS

RESULT 1					
ERB2_MOUSE					
ID	ERB2_MOUSE	STANDARD;	PRT;	245 AA.	
DT	P70424; Q61525;				
DT	15-DEC-1998 (Rel. 37, Created)				
DT	15-DEC-1998 (Rel. 37, Last sequence update)				
DT	28-FEB-2003 (Rel. 41, Last annotation update)				
DE	Receptor protein-tyrosine kinase erbB-2 (EC 2.7.1.112) (p185erbB2)				
DE	(NEU proto-oncogene) (C-erbB-2) (Fragments).				
GN	ERBB2 OR NEU.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE OF 1-149 FROM N.A.				
RC	STRAIN=CD-1; TISSUE=Uterus;				
RX	MEDLINE=97200814; PubMed=9048643;				
RA	Lim J., Dey S.K., Das S.K.;				
RT	"Differential expression of the erbB2 gene in the perimplantation				
RT	mouse uterus: potential mediator of signaling by epidermal growth				
RT	factor-like growth factors."				
RL	Endocrinology 138:1328-1337(1997).				
RN	[2]				
RP	SEQUENCE OF 150-245 FROM N.A.				
RX	MEDLINE=96069911; PubMed=7589796;				
RA	Moscoso L.M., Chu G.C., Gautam M., Noakes P.G., Merlie J.P.,				
RA	Sanes J.R.;				
RT	"Synapse-associated expression of an acetylcholine receptor-inducing				
RT	protein, ARIA/heresulin, and its putative receptors, ErbB2 and ErbB3,				
RT	in developing mammalian muscle."				
RL	Dev. Biol. 172:158-169(1995).				
RN	[3]				
RP	INTERACTION WITH PRKCAP.				
RX	MEDLINE=21226773; PubMed=11278603;				
RA	Jaulin-Bastard F., Saito H., Le Bivic A., Ollendorff V., Marchetto S.,				
RA	Birnbaum D., Borg J.-P.;				
RT	"The ERBB2/HER2 receptor differentially interacts with ERBIN and PICK1				
RT	PSD-95/DLG/ZO-1 domain proteins."				
RL	J. Biol. Chem. 276:15256-15263(2001).				
CC	-1- FUNCTION: Essential component of a neuroligin-receptor complex,				
CC	although neuroligins do not interact with it alone. GP30 is a				
CC	potential ligand for this receptor. Not activated by EGF, TGF-				
CC	alpha and amphiregulin.				
CC	-1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein				
CC	tyrosine phosphate.				
CC	-1- SUBUNIT: Heterodimer with each of the other ERBB receptors				
CC	(Potential). Interacts with PRKCAP.				
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.				
CC	-1- TISSUE SPECIFICITY: Expressed predominantly in uterine epithelial				
CC	cells. In the muscle, expression localizes to the synaptic sites				
CC	of muscle fibers.				
CC	-1- DEVELOPMENTAL STAGE: On days 1-4 of pregnancy, ERBB2 is detected				
CC	primarily in epithelial cells, the day 1 uterus showing the				
CC	highest accumulation. On day 5, the epithelium and the				
CC	decidualizing stromal cells around the implanting blastocyst				



FT MOD RES 1247 1247 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
 FT CARBOHYD 68 68 N-LINKED (GLCNAC) (POTENTIAL).  
 FT CARBOHYD 125 125 N-LINKED (GLCNAC) (POTENTIAL).  
 FT CARBOHYD 187 187 N-LINKED (GLCNAC) (POTENTIAL).  
 FT CARBOHYD 259 259 N-LINKED (GLCNAC) (POTENTIAL).  
 FT CARBOHYD 530 530 N-LINKED (GLCNAC) (POTENTIAL).  
 FT CARBOHYD 571 571 N-LINKED (GLCNAC) (POTENTIAL).  
 FT CARBOHYD 629 629 N-LINKED (GLCNAC) (POTENTIAL).  
 FT VARIANT 658 658 V -> E (IN ONCOGENIC NEU).  
 FT VARIANT 659 659 V -> E (IN ONCOGENIC NEU).  
 SQ SEQUENCE 1254 AA; 138252 MW; 974C3791C21F2BE1 CRC64;  
 Query Match 100.0%; Score 54; DB 1; Length 1254;  
 Best Local Similarity 100.0%; Pred. No. 0.011; Indels 0; Gaps 0;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EYLVPQGF 10  
 DB 1021 EYLVPQGF 1030  
 RESULT 3  
 ID ERB2\_HUMAN STANDARD; PRT; 1255 AA.  
 AC P04626;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DE Receptor protein-tyrosine kinase erbB-2 precursor (EC 2.7.1.112)  
 DE (p185erbB2) (NEU proto-oncogene) (C-erbB-2) (Tyrosine kinase-type cell  
 DE surface receptor HER2) (MLN 19).  
 GN ERBB2 OR HER2 OR NGL OR NEU.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86118663; PubMed=3003577;  
 RA Yamamoto T., Ikawa S., Akiyama T., Semba K., Nomura N., Miyajima N.,  
 RA Saito T., Toyoshima K.;  
 RT "Similarity of protein encoded by the human c-erbB-2 gene to  
 RT epidermal growth factor receptor.";  
 RL Nature 319:230-234(1986).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86070181; PubMed=2999974;  
 RA Coussens L., Yang-Feng T.L., Liao Y.C., Chen E., Gray A.,  
 RA McGrath J., Seeburg P.H., Libermann T.A., Schlessinger J.,  
 RA Francke U., Levinson A., Ullrich A.;  
 RT "Tyrosine kinase receptor with extensive homology to EGF receptor  
 RT shares chromosomal location with neu oncogene.";  
 RL Science 230:1132-1139(1985).  
 RN [3]  
 RP SEQUENCE OF 737-1031 FROM N.A.  
 RX MEDLINE=86016729; PubMed=2995967;  
 RA Semba K., Kanata N., Toyoshima K., Yamamoto T.;  
 RT "A v-erbB-related protooncogene, c-erbB-2, is distinct from the  
 RT c-erbB-1/epidermal growth factor-receptor gene and is amplified in a  
 RT human salivary gland adenocarcinoma.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 82:6497-6501(1985).  
 RN [4]  
 RP VARIANTS VAL-654 AND VAL-655.  
 RX MEDLINE=93194196; PubMed=8095488;  
 RA Ehsani A., Low J., Wallace R.B., Wu A.M.;  
 RT "Characterization of a new allele of the human ERBB2 gene by allele-  
 RT specific competition hybridization.";  
 RL Genomics 15:426-429(1993).  
 CC -1- FUNCTION: Essential component of a neuroligin-receptor complex,  
 CC although neuroligins do not interact with it alone. GP30 is a  
 CC potential ligand for this receptor. Not activated by EGF, TGF-  
 CC alpha and amphiregulin.  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein

CC tyrosine phosphate.  
 CC -1- SUBUNIT: Heterodimer with each of the other ERBB receptors  
 CC (POTENTIAL). Interacts with PRKCAP (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- PTM: Ligand-binding increases phosphorylation on tyrosine  
 CC residues (By similarity).  
 CC -1- POLYMORPHISM: There are four alleles due to the variations in  
 CC positions 654 and 655. Allele B1 (654-Ile-Ile-655) has a frequency  
 CC of 0.782; allele B2 (654-Ile-Val-655) has a frequency of 0.206;  
 CC allele B3 (654-Val-Val-655) has a frequency of 0.012.  
 CC -1- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.  
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 CC -----  
 CC EMBL; M11767; AAA35808.1; JOINED.  
 CC EMBL; M11761; AAA35808.1; JOINED.  
 CC EMBL; M11762; AAA35808.1; JOINED.  
 CC EMBL; M11763; AAA35808.1; JOINED.  
 CC EMBL; M11764; AAA35808.1; JOINED.  
 CC EMBL; M11765; AAA35808.1; JOINED.  
 CC EMBL; M11766; AAA35808.1; JOINED.  
 CC EMBL; M11730; AAA75493.1; JOINED.  
 CC EMBL; M12036; AAA35978.1; JOINED.  
 CC EMBL; X03363; CAA27060.1; JOINED.  
 CC PIR; A24571; A24571.  
 CC PDB; 1N82; 18-FEB-03.  
 CC PDB; 1ORI; 01-JAN-00.  
 CC Gene; HGNC:3430; ERBB2.  
 CC MIM; 164870; .  
 CC GO; GO:0005012; F:Neu/ErbB-2 receptor activity; TAS.  
 CC GO; GO:0004716; F:receptor signaling protein tyrosine kinase . . . TAS.  
 CC GO; GO:0008283; P:cell proliferation; TAS.  
 CC GO; GO:0007048; P:oncogenesis; TAS.  
 CC GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.  
 CC GO; GO:0006468; P:protein amino acid phosphorylation; TAS.  
 CC InterPro; IPR000494; EGFR\_L\_domain.  
 CC InterPro; IPR006211; Furin-like.  
 CC InterPro; IPR006212; Furin-repeat.  
 CC InterPro; IPR000719; Prot\_kinase.  
 CC InterPro; IPR001245; Tyr\_kinase.  
 CC InterPro; IPR004019; YLP\_motif.  
 CC Pfam; PF00757; Furin-like; 1.  
 CC Pfam; PF00069; Kinase; 1.  
 CC Pfam; PF01030; Recep\_L\_domain; 2.  
 CC Pfam; PF02757; YLP; 2.  
 CC PRINTS; PR00109; TYRKINASE.  
 CC ProDom; PD000001; Prot\_kinase; 1.  
 CC SMART; SM00261; FU; 4.  
 CC SMART; SM00219; Tyrc; 1.  
 CC PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 CC PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 CC PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
 CC Transmembrane; Glycoprotein; Multigene family; Receptor; Signal;  
 CC Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;  
 CC Polymorphism; 3D-structure.  
 CC SIGNAL 1 21  
 CC CHAIN 22 1255  
 CC DOMAIN 22 652  
 CC TRANSMEM 653 675  
 CC DOMAIN 676 1255  
 CC DOMAIN 720 987  
 CC NP\_BIND 726 734  
 CC BINDING 753 753  
 CC ACT\_SITE 845 845  
 CC DISULFID 195 204  
 CC DISULFID 199 212  
 CC DISULFID 220 227



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FT DISULFID 224 235 BY SIMILARITY.
FT DISULFID 236 244 BY SIMILARITY.
FT DISULFID 240 252 BY SIMILARITY.
FT DISULFID 255 264 BY SIMILARITY.
FT DISULFID 268 295 BY SIMILARITY.
FT DISULFID 299 311 BY SIMILARITY.
FT DISULFID 315 331 BY SIMILARITY.
FT DISULFID 334 338 BY SIMILARITY.
FT DISULFID 511 520 BY SIMILARITY.
FT DISULFID 515 528 BY SIMILARITY.
FT DISULFID 531 540 BY SIMILARITY.
FT DISULFID 544 560 BY SIMILARITY.
FT DISULFID 563 576 BY SIMILARITY.
FT DISULFID 567 584 BY SIMILARITY.
FT DISULFID 587 596 BY SIMILARITY.
FT DISULFID 600 623 BY SIMILARITY.
FT DISULFID 626 634 BY SIMILARITY.
FT DISULFID 630 642 BY SIMILARITY.
FT MOD_RES 1139 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 1248 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT CARBOHYD 68 68 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 124 124 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 187 187 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 259 259 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 530 530 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 571 571 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 629 629 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 654 654 I -> V (IN dbSNP:1801201).
FT VARIANT 655 655 /FTID-VAR_004077.
FT VARIANT 1170 1170 I -> V (IN dbSNP:1801200).
FT CONFLICT 1170 1170 P -> A (IN REF. 2).
FT SEQUENCE 1255 AA; 137909 MW; 39E9DFDA04DCF962 CRC64;

Query Match 100.08; Score 54; DB 1; Length 1255;
Best Local Similarity 100.08; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EBYLVPOQGF 10
Db 1021 EBYLVPOQGF 1030

RESULT 4
ERB2_RAT STANDARD; PRT; 1257 AA.
ID P06494;
DT 01-JAN-1988 (Rel. 06, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Receptor protein-tyrosine kinase erbB-2 precursor (EC 2.7.1.112)
DE (p185erbB2) (NEU proto-oncogene) (C-erbB-2) (Epidermal growth factor
DE receptor-related protein).
GN ERB2 OR NEU.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Neuroblastoma;
RX MEDLINE=86118662; PubMed=3945311;
RA Bargmann C.I., Hung M.-C., Weinberg R.A.;
RT "The new oncogene encodes an epidermal growth factor receptor-related
RL protein.";
RL Nature 319:226-230(1986).
RN [2]
RP SEQUENCE OF 852-905 FROM N.A.
RC TISSUE=Sciatic nerve;
RX MEDLINE=91222560; PubMed=2025425;
RA Lai C., Lemke G.;
RT "An extended family of protein-tyrosine kinase genes differentially
RT expressed in the vertebrate nervous system.";
```

```
RL Neuron 6:691-704(1991).
RN [3]
RP STRUCTURE BY NMR OF 650-668.
RX MEDLINE=92155181; PubMed=1346763;
RA Gullick W.J., Bottomley A.C., Lofte F.J., Doak D.G., Mulvey D.,
RA Newman R., Crumpton M.J., Sternberg M.J.E., Campbell I.D.;
RT "Three dimensional structure of the transmembrane region of the proto-
RL oncogenic and oncogenic forms of the neu protein.";
RL EMBO J. 11:43-48(1992).
CC -1- FUNCTION: Essential component of a neuroregulin-receptor complex,
CC although neuroregulins do not interact with it alone. GP30 is a
CC potential ligand for this receptor. Not activated by EGF, TGF-
CC alpha and amphiregulin.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
CC tyrosine phosphate.
CC -1- SUBUNIT: Heterodimer with each of the other ERBB receptors. The
CC constitutively activated oncogenic variant forms a homodimer.
CC Interacts with PRKCAP (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- PTM: Ligand-binding increases phosphorylation on tyrosine
CC residues (By similarity).
CC -1- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
CC
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CC
CC EMBL: X03362; CAA27059.1; ALT_INIT.
DR PDB; 1IJJ; 27-JUN-01.
DR InterPro; IPR000494; EGFR_L_domain.
DR InterPro; IPR006211; Furin-like.
DR InterPro; IPR006212; Furin_repeat.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR004019; YLP_motif.
DR Pfam; PF00757; Furin-like; 1.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF01030; Recep_L_domain; 2.
DR Pfam; PF02757; YLP; 2.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00261; FU; 4.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR Transmembrane; Glycoprotein; Multigene family; Receptor; Signal;
KW Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
KW Proto-oncogene; Disease mutation; 3D-structure.
FT SIGNAL 1 21
FT CHAIN 22 1257
FT DOMAIN 22 654 RECEPTOR PROTEIN-TYROSINE KINASE ERBB-2.
FT TRANSMEM 655 677 POTENTIAL.
FT DOMAIN 678 1257 POTENTIAL.
FT DOMAIN 159 369 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 473 646 CYS-RICH.
FT DOMAIN 722 989 CYS-RICH.
FT NP_BIND 728 736 PROTEIN KINASE.
FT BINDING 755 755 ATP (BY SIMILARITY).
FT ACT_SITE 847 847 BY SIMILARITY.
FT DISULFID 196 205 BY SIMILARITY.
FT DISULFID 200 213 BY SIMILARITY.
FT DISULFID 221 228 BY SIMILARITY.
FT DISULFID 225 236 BY SIMILARITY.
FT DISULFID 237 245 BY SIMILARITY.
FT DISULFID 241 253 BY SIMILARITY.
FT DISULFID 256 265 BY SIMILARITY.
FT DISULFID 269 296 BY SIMILARITY.
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FT DISULFID 300 312 BY SIMILARITY.
FT DISULFID 316 332 BY SIMILARITY.
FT DISULFID 335 339 BY SIMILARITY.
FT DISULFID 513 522 BY SIMILARITY.
FT DISULFID 517 530 BY SIMILARITY.
FT DISULFID 533 542 BY SIMILARITY.
FT DISULFID 546 562 BY SIMILARITY.
FT DISULFID 565 578 BY SIMILARITY.
FT DISULFID 569 586 BY SIMILARITY.
FT DISULFID 589 598 BY SIMILARITY.
FT DISULFID 602 625 BY SIMILARITY.
FT DISULFID 628 636 BY SIMILARITY.
FT DISULFID 632 644 BY SIMILARITY.
FT MOD_RES 1141 1141 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 1250 1250 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT CARBOHYD 68 68 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 532 532 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 573 573 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 631 631 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 661 661 V -> E (IN ONCOGENIC NEU).
SQ SEQUENCE 1257 AA; 138831 MW; 6129264583011402 CRC64;

Query Match 100.0%; Score 54; DB 1; Length 1257;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEVLVPOQGF 10
Db 1023 EEVLVPOQGF 1032

RESULT 5
EGFR_HUMAN STANDARD; PRT; 1210 AA.
AC P00533; O00688; O00732; P06268; Q14225; Q92795; Q9B252; Q9GEX1;
AC Q9H2C9; Q9H3C9; Q9UMD7; Q9UMDB; Q9UMG5;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Epidermal growth factor receptor precursor (EC 2.7.1.112) (Receptor
DE protein-tyrosine kinase ErbB-1).
GN EGFR OR ERBB1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=84219729; PubMed=6328312;
RA Ullrich A., Coussens L., Hayflick J.S., Dull T.J., Gray A., Tam A.W.,
RA Lee J., Yarden Y., Libermann T.A., Schlessinger J., Downward J.,
RA Mayes E.L.V., Whittle N., Waterfield M.D., Seeburg P.H.;
RA "Human epidermal growth factor receptor cDNA sequence and aberrant
RT expression of the amplified gene in A431 epidermoid carcinoma cells.";
RL Nature 309:418-425(1984).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX MEDLINE=84219729; PubMed=6328312;
RA Ullrich A., Coussens L., Hayflick J.S., Dull T.J., Gray A., Tam A.W.,
RA Lee J., Yarden Y., Libermann T.A., Schlessinger J., Downward J.,
RA Mayes E.L.V., Whittle N., Waterfield M.D., Seeburg P.H.;
RA "Human epidermal growth factor receptor cDNA sequence and aberrant
RT expression of the amplified gene in A431 epidermoid carcinoma cells.";
RL Nature 309:418-425(1984).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX MEDLINE=95382957; PubMed=7654368;
RA Ilekis J.V., Stark B.C., Scoccia B.;
RA "Possible role of variant RNA transcripts in the regulation of
RT epidermal growth factor receptor expression in human placenta.";
RL Mol. Reprod. Dev. 41:149-156(1995).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX MEDLINE=97078686; PubMed=8918811;
RA Reiter J.L., Maible N.J.;
RA "A 1.8 kb alternative transcript from the human epidermal growth
RT factor receptor gene encodes a truncated form of the receptor.";
RL Nucleic Acids Res. 24:4050-4056(1996).

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RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX MEDLINE=97256547; PubMed=9103388;
RA Ilekis J.V., Gariti J., Niederberger C., Scoccia B.;
RA "Expression of a truncated epidermal growth factor receptor-like
RT protein (TEGFR) in ovarian cancer.";
RL Gynecol. Oncol. 65:36-41(1997).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORMS 3 AND 4).
RX MEDLINE=91100872; PubMed=11161793;
RA Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E., Danielsen A.J.,
RA Schehl Sincilar C., Pearsall R.S., Green P.J., Yee D., Lampland A.L.,
RA Balasubramaniam S., Crossley T.D., Magnuson T.R., James C.D.,
RA Maible N.J.;
RA "Comparative genomic sequence analysis and isolation of human and
RT mouse alternative EGFR transcripts encoding truncated receptor
RT isoforms.";
RL Genomics 71:1-20(2001).
RN [6]
RP SEQUENCE OF 575-687 FROM N.A.
RA Reiter J.L., Threadgill D.W., Danielsen A.J., Schehl C.M.,
RA Lampland A.L., Balasubramaniam S., Crossley T.O., Magnuson T.R.,
RA Maible N.J.;
RA "Human and mouse alternative EGFR transcripts encoding only the
RT extracellular domain of the receptor.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE OF 713-924 FROM N.A.
RX MEDLINE=84196372; PubMed=6326261;
RA Lin C.R., Chen W.S., Krueger W., Stolarsky L.S., Weber W.,
RA Evans R.M., Verma I.M., Gill G.N., Rosenfeld M.G.;
RA "Expression cloning of human EGF receptor complementary DNA: gene
RT amplification and three related messenger RNA products in A431
RT cells.";
RL Science 224:843-848(1984).
RN [8]
RP SEQUENCE OF 150-962 FROM N.A.
RX MEDLINE=84245835; PubMed=6330563;
RA Xu Y.H., Ishii S., Clark A.J.L., Sullivan M., Wilson R.K., Ma D.P.,
RA Roe B.A., Merlino G.T., Pastan I.;
RA "Human epidermal growth factor receptor cDNA is homologous to a
RT variety of RNAs overproduced in A431 carcinoma cells.";
RL Nature 309:806-810(1984).
RN [9]
RP SEQUENCE OF 1028-1210 FROM N.A.
RX MEDLINE=85046483; PubMed=6093780;
RA Simmen F.A., Gope M.L., Schulz T.Z., Wright D.A., Carpenter G.,
RA O'Malley B.W.;
RA "Isolation of an evolutionarily conserved epidermal growth factor
RT receptor cDNA from human A431 carcinoma cells.";
RL Biochem. Biophys. Res. Commun. 124:125-132(1984).
RN [10]
RP SEQUENCE OF 1-29 FROM N.A.
RX MEDLINE=88217333; PubMed=3329716;
RA Haley J.D., Whittle N., Bennett P., Kinchington D., Ullrich A.,
RA Waterfield M.D.;
RA "The human EGF receptor gene: structure of the 110 kb locus and
RT identification of sequences regulating its transcription.";
RL Oncogene Res. 1:375-396(1987).
RN [11]
RP SEQUENCE OF 1-29 FROM N.A.
RX MEDLINE=91107677; PubMed=1988448;
RA Haley J.D., Waterfield M.D.;
RA "Contributory effects of de novo transcription and premature
RT transcript termination in the regulation of human epidermal growth
RT factor receptor proto-oncogene RNA synthesis.";
RL J. Biol. Chem. 266:1746-1753(1991).
RN [12]
RP SEQUENCE OF 1-29 FROM N.A.
RX MEDLINE=85270438; PubMed=2991899;
RA Ishii S., Xu Y.H., Stratton R.H., Roe B.A., Merlino G.T., Pastan I.;

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RT "Characterization and sequence of the promoter region of the human.  
 RL epidermal growth factor receptor gene.";  
 RN Proc. Natl. Acad. Sci. U.S.A. 82:4920-4924(1985).  
 RP SEQUENCE OF 540.  
 RA Kohda D.;  
 RL Submitted (SEP-1997) to the SWISS-PROT data bank.  
 RN RECEPTOR ACTIVITY.  
 RP MEDLINE-84191554; PubMed-6325948;  
 RA Mroczkowski B., Mosig G., Cohen S.;  
 RT "ATP-stimulated interaction between epidermal growth factor receptor  
 RL and supercoiled DNA.";  
 RN Nature 309:270-273(1984).  
 RP PHOSPHORYLATION.  
 RA Margolis B.L., Lax I., Kris R., Dombalagian M., Honegger A.M.,  
 RA Hawk R., Givol D., Ullrich A., Schlessinger J.;  
 RT "All autophosphorylation sites of epidermal growth factor (EGF)  
 RL receptor and HER2/neu are located in their carboxyl-terminal tails.  
 RN Identification of a novel site in EGF receptor.";  
 RL J. Biol. Chem. 264:10667-10671(1989).  
 RN CARBOHYDRATE-LINKAGE SITES ASN-128; ASN-175; ASN-413; ASN-444 AND  
 RP ASN-528.  
 RA Smith K.D., Davies M.J., Bailey D., Renouf D.V., Hounsell E.F.;  
 RT "Analysis of the glycosylation patterns of the extracellular domain of  
 RL the epidermal growth factor receptor expressed in Chinese hamster  
 RN ovary fibroblasts.";  
 RP Growth Factors 13:121-132(1996).  
 RA CARBOHYDRATE-LINKAGE SITES ASN-56; ASN-352; ASN-361; ASN-568 AND  
 RP ASN-603.  
 RA MEDLINE-20198209; PubMed-10731668;  
 RT Sato C., Kim J.-H., Abe Y., Saito K., Yokoyama S., Kohda D.;  
 RL "Characterization of the N-oligosaccharides attached to the atypical  
 RN Asn-X-Cys sequence of recombinant human epidermal growth factor  
 RL receptor.";  
 RN J. Biol. Chem. 273:11150-11157(1998).  
 RP REVIEW.  
 RA MEDLINE-87297456; PubMed-3039909;  
 RT Carpenter G.;  
 RL "Receptors for epidermal growth factor and other polypeptide  
 RN mitogens.";  
 RA Annu. Rev. Biochem. 56:881-914(1987).  
 RP INTERACTION WITH RIPK1.  
 RA PubMed-11116146;  
 RL Habib A.A., Chatterjee S., Park S.-K., Ratan R.R., Lefebvre S.,  
 RA Vartanian T.;  
 RT "The epidermal growth factor receptor engages receptor interacting  
 RL protein and nuclear factor-kappa B (NF-kappa B)-inducing kinase to  
 RT activate NF-kappa B. Identification of a novel receptor-tyrosine  
 RL kinase signalosome.";  
 RN J. Biol. Chem. 276:8865-8874(2001).  
 CC -!- FUNCTION: Receptor for EGF, but also for other members of the EGF  
 CC family, as TGF-alpha, amphiregulin, betacellulin, heparin-binding  
 CC EGF-like growth factor, GP30 and vaccinia virus growth factor. Is  
 CC involved in the control of cell growth and differentiation.  
 CC -!- FUNCTION: Isoform 2/truncated isoform may act as an antagonist.  
 CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
 CC tyrosine phosphate.  
 CC -!- SUBUNIT: Binds RIPK1.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Isoform 2 is

CC secreted  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=4;  
 CC Name=1; Synonyms=pl170;  
 CC IsoId=P00533-1; Sequence=Displayed;  
 CC Name=2; Synonyms=p60, Truncated, TEGFR;  
 CC IsoId=P00533-2; Sequence=VSP\_002887, VSP\_002888;  
 CC Name=3; Synonyms=pl10;  
 CC IsoId=P00533-3; Sequence=VSP\_002889, VSP\_002890;  
 CC Name=4;  
 CC IsoId=P00533-4; Sequence=VSP\_002891, VSP\_002892;  
 CC -!- TISSUE SPECIFICITY: Expressed in placenta. Isoform 2 is also  
 CC expressed in ovarian cancers.  
 CC -!- MISCELLANEOUS: Binding of EGF to the receptor leads to  
 CC dimerization, internalization of the EGF-receptor complex,  
 CC induction of the tyrosine kinase activity, stimulation of cell DNA  
 CC Query Match 92.6%; Score 50; DB 1; Length 1210;  
 CC Best Local Similarity 80.0%; Pred. No. 0.066;  
 CC Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EYLVPPQGF 10  
 Db 1014 DEVLPQGF 1023  
 RESULT 6  
 EGF\_MOUSE  
 ID EGF\_MOUSE STANDARD; PRT; 1210 AA.  
 AC Q01279;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Epidermal growth factor receptor precursor (EC 2.7.1.112).  
 GN EGF.  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c; TISSUE=Liver;  
 RX MEDLINE=93026370; PubMed=1408137;  
 RA Avivi A., Skorecki K., Yayon A., Givol D.;  
 RT "Promoter region of the murine fibroblast growth factor receptor 2  
 RL (bek/KGFR) gene.";  
 RN Oncogene 7:1957-1962(1992).  
 RP [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c, and CD-1; TISSUE=Decidua, and Liver;  
 RX MEDLINE=93126380; PubMed=7678348;  
 RA Paria B.C., Das S.K., Andrews G.K., Dey S.K.;  
 RT "Expression of the epidermal growth factor receptor gene is regulated  
 RL in mouse blastocysts during delayed implantation.";  
 RN Proc. Natl. Acad. Sci. U.S.A. 90:55-59(1993).  
 RP [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c; TISSUE=Liver;  
 RX Hibbs M.L.;  
 RN Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.  
 RP [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=B6/C3; TISSUE=Liver;  
 RX MEDLINE=94170986; PubMed=8125255;  
 RA Luetteke N.C., Phillips H.K., Qiu T.H., Copeland N.G., Earp H.S.,  
 RA Jenkins N.A., Lee D.C.;  
 RT "The mouse waved-2 phenotype results from a point mutation in the EGF  
 RL receptor tyrosine kinase.";  
 RN Genes Dev. 8:399-413(1994).  
 RP [5]  
 RP SEQUENCE OF 1-714 FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=91232866; PubMed=2030916;



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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch))

CC EMBL; M13179; AAA42401.1; -  
 DR PIR; A25231; TVFVEB.  
 DR HSP; P11362; IFGK.  
 DR InterPro; IPR000719; Prot\_Kinase.  
 DR Pfam; PF00069; pkinase; 1.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD000001; Prot\_Kinase; 1.  
 DR SMART; SM00219; TyrKc; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
 KW Transferase; Tyrosine-protein kinase; ATP-binding; Oncogene;  
 KW Glycoprotein; Phosphorylation.  
 FT DOMAIN 132 399  
 FT NP\_BIND 138 146 PROTEIN KINASE.  
 FT BINDING 165 165 ATP (BY SIMILARITY).  
 FT ACT\_SITE 257 257 ATP (BY SIMILARITY).  
 FT VARIANT 270 270 BY SIMILARITY.  
 FT SEQUENCE 540 AA; 60412 MW; 5853297AA068B65D CRC64;  
 SQ

Query Match 85.2%; Score 46; DB 1; Length 540;  
 Best Local Similarity 80.0%; Pred. No. 0.19;  
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 EEVLVPQGGF 10  
 :|||||  
 DB 434 DEYLVPHQGF 443

## RESULT 8

ERBB\_AVIER  
 ID ERBB\_AVIER STANDARD; PRT; 604 AA.  
 AC P00535;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Tyrosine-protein kinase transforming protein erbB (EC 2.7.1.112).  
 GN V-ERBB.  
 OS Avian erythroblastosis virus (strain ES4).  
 OC Viruses; Retroviral viruses; Retroviridae; Avian type C retroviruses.  
 OX NCBI\_TaxID=79685;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H;  
 RX MEDLINE=84026539; PubMed=6313229;  
 RA Yamamoto T., Nishida T., Miyajima N., Kawai S., Ooi T., Toyoshima K.;  
 RT "The erbB gene of avian erythroblastosis virus is a member of the src  
 RT gene family.";  
 RL Cell 35:71-78(1983).  
 RN [2]  
 RP SEQUENCE OF 1-152 FROM N.A.  
 RX MEDLINE=84223957; PubMed=6328658;  
 RA Debouire B., Henry C., Benalissa M., Biserte G., Claverie J.-M.,  
 RA Saule S., Martin P., Stehelin D.;  
 RT "Sequencing the erbA gene of avian erythroblastosis virus reveals a  
 RT new type of oncogene.";  
 RL Science 224:1456-1459(1984).  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein  
 CC tyrosine phosphate.  
 CC -1- DISEASE: THE V-ERBB ONCOGENE TRANSFORMS AVIAN FIBROBLASTS AND  
 CC ERYTHROBLASTS IN CULTURE AND INDUCES SARCOMAS AND ERYTHROLEUKEMIAS  
 CC IN CHICKENS.  
 CC -1- MISCELLANEOUS: V-ERBB IS A TRUNCATED AND MUTATED VERSION OF THE  
 CC RECEPTOR FOR EPIDERMAL GROWTH FACTOR.  
 CC -1- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.

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CC EMBL; K02006; AAA42394.1; ALT\_INIT.

DR EMBL; K01216; AAA42400.1; -  
 DR PIR; A00644; TVYUH.  
 DR HSP; P11362; IFGK.  
 DR InterPro; IPR000719; Prot\_Kinase.  
 DR Pfam; PF00069; pkinase; 1.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD000001; Prot\_Kinase; 1.  
 DR SMART; SM00219; TyrKc; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
 KW Transferase; Tyrosine-protein kinase; ATP-binding; Oncogene;  
 KW Glycoprotein; Phosphorylation.  
 FT DOMAIN 132 399  
 FT NP\_BIND 138 146 PROTEIN KINASE.  
 FT BINDING 165 165 ATP (BY SIMILARITY).  
 FT ACT\_SITE 257 257 ATP (BY SIMILARITY).  
 FT CONFLICT 29 29 R -> W (IN REF. 2).  
 FT CONFLICT 140 140 S -> F (IN REF. 2).  
 FT CONFLICT 146 146 I -> V (IN REF. 2).  
 FT SEQUENCE 604 AA; 67633 MW; 76BECDD06745D609 CRC64;  
 SQ

Query Match 85.2%; Score 46; DB 1; Length 604;  
 Best Local Similarity 80.0%; Pred. No. 0.21;  
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 EEVLVPQGGF 10  
 :|||||  
 DB 434 DEYLVPHQGF 443

## RESULT 9

ERBB\_ALV  
 ID ERBB\_ALV STANDARD; PRT; 634 AA.  
 AC P00534;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Tyrosine-protein kinase transforming protein erbB (EC 2.7.1.112).  
 GN V-ERBB.  
 OS Avian leukosis virus.  
 OC Viruses; Retroviral viruses; Retroviridae; Alpharetrovirus.  
 OX NCBI\_TaxID=11864;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85228222; PubMed=2988784;  
 RA Nilsen T.W., Maroney P.A., Goodwin R.G., Rottman F.M.,  
 RA Crittenden L.B., Raines M.A., Kung H.-J.;  
 RT "c-erbB activation in ALV-induced erythroblastosis: novel RNA  
 RT processing and promoter insertion result in expression of an  
 RT amino-truncated EGF receptor.";  
 RL Cell 41:719-726(1985).  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein  
 CC tyrosine phosphate.  
 CC -1- MISCELLANEOUS: THIS PROTEIN IS PRODUCED BY ERYTHROLEUKEMIA CELLS  
 CC IN CHICKS WHICH HAVE BEEN INJECTED WITH THE AVIAN LEUKOSIS VIRUS  
 CC AND SUBSEQUENTLY DEVELOP LEUKEMIA. THE LEUKEMIAS ARE INDUCED BY  
 CC THE INSERTION OF RETROVIRAL PROMOTER ELEMENTS IN OR NEAR THE  
 CC C-ERBB GENE, WHICH LEADS TO C-ERBB ACTIVATION.  
 CC -1- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A GAG-ENV-ERBB  
 CC PROTEIN.  
 CC -1- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.

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CC -----
CC EMBL: M10066; AAA48763.1; ALT_INIT.
CC HSPF: P11362; IFGK.
CC InterPro: IPR000719; Prot_kinase.
CC InterPro: IPR001245; Tyr_pkinase.
CC Pfam: PF00069; pkinase; 1.
CC PRINTS: PR0109; TYRKINASE.
CC ProDom: PD000001; Prot_kinase; 1.
CC SMART: SM00219; TyrRC; 1.
CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
CC PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
CC Transferrase: Tyrosine-protein kinase; ATP-binding; Oncogene;
KW Glycoprotein; Phosphorylation.
FT DOMAIN 132 399
FT NP_BIND 138 146 ATP (BY SIMILARITY).
FT BINDING 165 165 ATP (BY SIMILARITY).
FT ACT_SITE 257 257 BY SIMILARITY.
SQ SEQUENCE 634 AA; 70891 MW; E705E33A0BE01FCC CRC64;

Query Match 85.2%; Score 46; DB 1; Length 634;
Best Local Similarity 80.0%; Pred. No. 0.22;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EYLVPQOGF 10
DB 434 DEYLVPHQGF 443

RESULT 10
YH73_SYNY3
ID YH73_SYNY3 STANDARD; PRT; 232 AA.
AC P73623;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein sl11773.
GN SL11773.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kottani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hirosewa M., Sugitani M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA Shimo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
CC -!- SIMILARITY: BELONGS TO THE PIRIN FAMILY.
CC -----
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CC -----
CC EMBL: D90908; BAAL7668.1; -.
CC PIR: S77110; S77110.

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DR InterPro: IPR007113; Cupin_sup.
DR InterPro: IPR003829; DUF209.
DR Pfam: PF03678; Pirin; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 232 AA; 25700 MW; 09B9DCC65352A470 CRC64;

Query Match 70.4%; Score 38; DB 1; Length 232;
Best Local Similarity 60.0%; Pred. No. 3.2;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EYLVPQOGF 10
DB 45 EDYIAPGQGF 54

RESULT 11
ERB4_MOUSE
ID ERB4_MOUSE STANDARD; PRT; 95 AA.
AC Q61527;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Receptor protein-tyrosine kinase erbB-4 (EC 2.7.1.112) (Fragments).
GN ERB4 OR MER4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE OF 1-27 FROM N.A. (ISOFORMS JM-A AND JM-B).
RC TISSUE=Heart, and Kidney;
RX MEDLINE=97476287; PubMed=9334263;
RA Elenius K., Corfas G., Paul S., Choi C.J., Rio C., Plowman G.D.,
RA Klagsbrun M.;
RT "A novel juxtamembrane domain isoform of HER4/ErbB4. Isoform-specific
RT tissue distribution and differential processing in response to
RT phorbol ester.";
RL J. Biol. Chem. 272:26761-26768(1997).
RN [2]
RP SEQUENCE OF 28-95 FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=96069911; PubMed=7589796;
RA Moscote L.M., Chu G.C., Gautam M., Noakes P.G., Merlie J.P.,
RA Sanes J.R.;
RT "Synapse-associated expression of an acetylcholine receptor-inducing
RT protein, ARIA/herregulin, and its putative receptors, ErbB2 and ErbB3,
RT in developing mammalian muscle.";
RL Dev. Biol. 172:158-169(1995).
CC -!- FUNCTION: Specifically binds and is activated by neuregulins, NRG-
CC 2, NRG-3, heparin-binding EGF-LIKE growth factor, betacellulin and
CC NTAK. Interaction with these factors induces cell differentiation.
CC Not activated by EGF, TGF-A, and amphiregulin (by similarity).
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -!- SUBUNIT: Homodimer or heterodimer with each of the other ERBB
CC receptors. Interacts with the PDZ domain of the syntrophin SNTB2
CC (by similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Comment=The 2 isoforms differ functionally in their response to
CC phorbol ester: isoform JM-A is processed but not isoform JM-B.
CC So, they respectively represent cleavable and noncleavable
CC forms of the receptor. Both isoforms are expressed in
CC cerebellum, cerebral cortex, spinal cord, medulla oblongata,
CC and eye, but the kidney expresses solely isoform JM-A and the
CC heart solely isoform JM-B;
CC Name=JM-A;
CC IsoId=Q61527-1; Sequence=Displayed;
CC Name=JM-B;
CC IsoId=Q61527-2; Sequence=VSP_002896;
CC -!- PTM: Ligand-binding increases phosphorylation on tyrosine
CC residues.

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CC CC -1- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
CC -----
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC CC EMBL: L47241; AAA93534.1;
CC DR MGD: MGI-104771; ErbB4.
CC DR GO: GO:0043165; P:cell fate commitment; IDA.
CC DR GO: GO:0007507; P:heart development; IMP.
CC DR GO: GO:0007399; P:neurogenesis; IMP.
CC DR InterPro: IPR000719; Prot_kinase.
CC DR InterPro: IPR001245; Tyr_kinase.
CC DR PROSITE: PS00107; PROTEIN_KINASE_ATP; PARTIAL.
CC DR PROSITE: PS00109; PROTEIN_KINASE_TYR; PARTIAL.
CC DR PROSITE: PS00111; PROTEIN_KINASE_DOM; PARTIAL.
CC DR Transmembrane; Glycoprotein; Multigene family; Receptor; Transferase;
CC KW Tyrosine-protein kinase; ATP-binding; Phosphorylation;
CC KW Alternative splicing.
CC FT NON_TER 1 1
CC FT NON_CONS 27 28
CC FT VARSPLIC 3 25
CC FT FT
CC FT FT
CC FT FT
CC SQ SEQUENCE 95 AA; 10524 MW; B43D0E9591744D8 CRC64;
CC
CC Query Match 68.5%; Score 37; DB 1; Length 95;
CC Best Local Similarity 100.0%; Pred. No. 2;
CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 1 EBYLVPQ 7
CC DB 29 EBYLVPQ 35
CC
CC RESULT 12
CC TGM2_BOVIN
CC ID TGM2_BOVIN STANDARD; PRT; 687 AA.
CC AC P51176;
CC DT 01-OCT-1996 (Rel. 34, Created)
CC DT 01-OCT-1996 (Rel. 34, Last sequence update)
CC DT 15-SEP-2003 (Rel. 42, Last annotation update)
CC DE Protein-glutamine gamma-glutamyltransferase (EC 2.3.2.13) (Tissue
CC transglutaminase) (TGase C) (TGC) (TG(C)) (Transglutaminase 2).
CC GN TGM2.
CC OS Bos taurus (Bovine).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
CC OC Bovidae; Bovinae; Bos.
CC OX NCBI_TaxID=9913;
CC RN [1]
CC RP SEQUENCE FROM N.A., AND SEQUENCE OF 79-95; 157-166; 242-251 AND
CC 581-587.
CC RC TISSUE=Artery;
CC RX MEDLINE=92037637; PubMed=1682150;
CC RA Nakanishi K., Nara K., Hagiwara H., Aoyama Y., Ueno H., Hirose S.;
CC RT "Cloning and sequence analysis of cDNA clones for bovine aortic-
CC endothelial-cell transglutaminase."
CC RL Eur. J. Biochem. 202:15-21(1991).
CC CC -1- FUNCTION: CATALYZES THE CROSS-LINKING OF PROTEINS AND THE
CC CONJUGATION OF POLYAMINES TO PROTEINS.
CC CC -1- CATALYTIC ACTIVITY: Protein glutamine + alkylamine -> protein N(5)-
CC alkylglutamine + NH(3).
CC CC -1- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC CC -1- SUBUNIT: Monomer (By similarity).
CC CC -1- TISSUE SPECIFICITY: HIGHEST LEVELS ARE DETECTED IN THE LUNG. LOWER
CC LEVELS ARE FOUND IN THE LIVER, SPLEEN AND HEART, BUT NOT IN THE
CC BRAIN.

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CC CC -1- INDUCTION: By retinoic acid.
CC CC -1- SIMILARITY: BELONGS TO THE TRANSGLUTAMINASE FAMILY.
CC -----
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC CC EMBL: X60686; CA443097.1;
CC DR PIR: S19680; SI9680.
CC DR HSP: P00488; IORX.
CC DR InterPro: IPR001102; GluttransfG.
CC DR InterPro: IPR002931; Transglutaminase_like.
CC DR Pfam: PF01841; Transglut_core; 1.
CC DR Pfam: PF00927; Transglutamin_C; 2.
CC DR Pfam: PF00868; Transglutamin_N; 1.
CC DR SMART: SM00460; TGC; 1.
CC DR PROSITE: PS00547; TRANSGLUTAMINASES; 1.
CC KW Transferase; Acyltransferase; Calcium-binding.
CC FT ACT_SITE 277 277 BY SIMILARITY.
CC FT ACT_SITE 335 335 BY SIMILARITY.
CC FT ACT_SITE 358 358 BY SIMILARITY.
CC FT METAL 398 398 CALCIUM (BY SIMILARITY).
CC FT METAL 400 400 CALCIUM (BY SIMILARITY).
CC FT METAL 447 447 CALCIUM (BY SIMILARITY).
CC FT METAL 452 452 CALCIUM (BY SIMILARITY).
CC SQ SEQUENCE 687 AA; 77112 MW; 7BBA00F15E779944 CRC64;
CC
CC Query Match 68.5%; Score 37; DB 1; Length 687;
CC Best Local Similarity 60.0%; Pred. No. 15;
CC Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
CC
CC QY 1 EBYLVPQGF 10
CC DB 157 QEYVLTQGF 166
CC
CC RESULT 13
CC TGM2_HUMAN
CC ID TGM2_HUMAN STANDARD; PRT; 687 AA.
CC AC P21980; Q16436; Q9BTN7; Q9UH35;
CC DT 01-AUG-1991 (Rel. 19, Created)
CC DT 28-FEB-2003 (Rel. 41, Last sequence update)
CC DT 15-SEP-2003 (Rel. 42, Last annotation update)
CC DE Protein-glutamine gamma-glutamyltransferase (EC 2.3.2.13) (Tissue
CC transglutaminase) (TGase C) (TGC) (TG(C)) (Transglutaminase 2)
CC (TGase-H).
CC GN TGM2.
CC OS Homo sapiens (Human).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CC OX NCBI_TaxID=9606;
CC RN [1]
CC RP SEQUENCE FROM N.A. (ISOFORM 1), AND PARTIAL SEQUENCE.
CC RC TISSUE=Endothelial cells;
CC RX MEDLINE=91093168; PubMed=1670766;
CC RA Gentile V., Saydak M., Chioce E.A., Akande O., Birckbichler P.J.,
CC Lee K.N., Stein J.P., Davies P.J.A.;
CC RT "Isolation and characterization of cDNA clones to mouse macrophage
CC and human endothelial cell tissue transglutaminases."
CC RL J. Biol. Chem. 266:478-483(1991).
CC RN [2]
CC RP SEQUENCE FROM N.A. (ISOFORM 2).
CC RX MEDLINE=93054562; PubMed=1358880;
CC RA Fraij B.M., Birckbichler P.J., Patterson M.K. Jr., Lee K.N.,
CC Gonzales R.A.;
CC RT "A retinoic acid-inducible mRNA from human erythroleukemia cells
CC encodes a novel tissue transglutaminase homologue."
CC RL J. Biol. Chem. 267:22616-22623(1992).
CC RN [3]

```







lung, salivary gland, and pancreas.  
 -1- PTM: Ligand-binding increases phosphorylation on tyrosine residues.  
 -1- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.  
 -----  
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 -----  
 EMBL: L07868; AAB59446.1; -  
 PIR: A47253; A47253.  
 HSSP: P11362; 1FGK.  
 Genew: HGNC:3432; ERBB4.  
 MIM: 600543; -  
 GO: GO:0005887; C: Integral to plasma membrane; TAS.  
 GO: GO:0008283; P: cell proliferation; TAS.  
 GO: GO:0007275; P: development; TAS.  
 GO: GO:0007048; P: oncogenesis; TAS.  
 InterPro: IPR000494; EGFR\_L\_domain.  
 InterPro: IPR008211; Furin-like.  
 InterPro: IPR006212; Furin-repeat.  
 InterPro: IPR007119; Prot\_kinase.  
 InterPro: IPR001245; Tyr\_kinase.  
 InterPro: IPR004019; YLP\_motif.  
 Pfam: PF00757; Furin-like; 1.  
 Pfam: PF00069; kinase; 1.  
 Pfam: PF01030; Recep\_L\_domain; 2.  
 Pfam: PF02757; YLP; 2.  
 PRINTS: PR00109; TYRKINASE.  
 ProDom: PD000001; Prot\_kinase; 1.  
 SMART: SM00261; FU; 5.  
 SMART: SM00219; Tykrc; 1.  
 PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
 PROSITE: PS00109; PROTEIN\_KINASE\_TYR; 1.  
 PROSITE: PS00011; PROTEIN\_KINASE\_DOM; 1.  
 Transmembrane: Glycoprotein; Multigene family; Receptor; Signal;  
 KW Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;  
 KW Alternative splicing.  
 FT SIGNAL 1 25  
 FT CHAIN 26 1308  
 FT DOMAIN 26 651  
 FT TRANSMEM 652 675  
 FT DOMAIN 676 1308  
 FT DOMAIN 186 334  
 FT DOMAIN 496 633  
 FT DOMAIN 718 985  
 FT NP\_BIND 724 732  
 FT BINDING 751 751  
 FT ACT\_SITE 843 843  
 FT DISULFID 189 197  
 FT DISULFID 193 205  
 FT DISULFID 213 221  
 FT DISULFID 217 229  
 FT DISULFID 230 238  
 FT DISULFID 234 246  
 FT DISULFID 249 258  
 FT DISULFID 262 289  
 FT DISULFID 293 304  
 FT DISULFID 308 323  
 FT DISULFID 326 330  
 FT DISULFID 503 512  
 FT DISULFID 507 520  
 FT DISULFID 523 532  
 FT DISULFID 536 552  
 FT DISULFID 555 569  
 FT DISULFID 559 577  
 FT DISULFID 580 589  
 FT DISULFID 593 614  
 FT DISULFID 617 625

FT DISULFID 621 633 BY SIMILARITY.  
 FT MOD\_RES 1162 1182 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
 FT MOD\_RES 1188 1188 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
 FT MOD\_RES 1258 1258 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
 FT MOD\_RES 1284 1284 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
 FT CARBOHYD 138 138 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 174 174 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 181 181 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 253 253 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 358 358 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 410 410 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 473 473 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 495 495 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 548 548 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 576 576 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 620 620 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT VARSPLIC 626 648 NGPTSHDCIYPTWGTGHTLPHQA -> IGSIEDICIGLMD  
 (in isoform JM-B).  
 FT FT /FTid=VSP\_002895.  
 SQ SEQUENCE 1308 AA; 146807 MW; 5E4AE80985D88761 CRC64;

Query Match 68.5%; Score 37; DB 1; Length 1308;  
 Best Local Similarity 100.0%; Pred. No. 28;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEVLVPQ 7  
 |||||  
 Db 1020 EEVLVPQ 1026

Search completed: July 28, 2003, 17:04:13  
 Job time : 24 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 28, 2003, 17:00:40 ; Search time 40 Seconds  
(without alignments)  
24.042 Million cell updates/sec

Title: US-09-930-125-3  
Perfect score: 54  
Sequence: 1 EYLVPPQGGF 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_76: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	54	100.0	1254	2 I48161	p-185 precursor -
2	54	100.0	1255	1 A24571	protein-tyrosine k
3	54	100.0	1260	1 TVRTWU	protein-tyrosine k
4	50	92.6	1210	1 GQHUE	epidermal growth f
5	50	92.6	1210	2 A53183	epidermal growth f
6	46	85.2	540	1 TVFVEB	protein-tyrosine k
7	46	85.2	540	2 B44776	protein-tyrosine k
8	46	85.2	544	2 S35745	kinase-related tra
9	46	85.2	545	2 S00727	protein-tyrosine k
10	46	85.2	604	1 TVYUHH	protein-tyrosine k
11	46	85.2	698	1 TVFVLV	protein-tyrosine k
12	46	85.2	1223	1 TVCHLV	epidermal growth f
13	38	70.4	232	2 S77110	hypothetical prote
14	37	68.5	349	2 S68092	protein-glutamine
15	37	68.5	428	2 A61611	probable proteinase
16	37	68.5	428	2 A11248	probable proteinase
17	37	68.5	548	2 A43502	protein-glutamine
18	37	68.5	687	1 A39045	protein-glutamine
19	37	68.5	687	2 S19680	protein-glutamine
20	37	68.5	691	1 A29996	protein-glutamine
21	37	68.5	751	2 T20733	hypothetical prote
22	37	68.5	1308	2 A47253	epidermal growth f
23	36	66.7	436	2 E90261	hypothetical prote
24	35	64.8	123	2 T50142	probable phosphogl
25	35	64.8	209	2 T37764	probable phosphogl
26	35	64.8	391	2 B48085	CAU1 protein - yea
27	35	64.8	687	1 B39045	protein-glutamine
28	35	64.8	917	1 R0MUNH	nitrate reductase
29	35	64.8	1242	2 S51246	probable DNA repai

30	34	63.0	262	2 B71817	hypothetical prote
31	34	63.0	330	2 D75032	anion transporting
32	34	63.0	431	2 AG2105	4-aminobutyrate am
33	34	63.0	432	2 D95369	conserved hypothet
34	34	63.0	518	2 B86372	protein F508.34 li
35	34	63.0	541	2 A48717	glutamate formimid
36	34	63.0	598	2 S55014	NADH2 dehydrogenas
37	34	63.0	768	2 JC7352	glucose-regulated
38	34	63.0	988	1 TOEC21	transposase - Esch
39	34	63.0	997	2 S73556	MG414 homolog C12
40	34	63.0	1019	2 JC7538	neuronal different
41	34	63.0	1097	2 A29943	Toll protein precu
42	34	63.0	2290	1 GNNYE	genome polyprotein
43	34	63.0	2292	1 GNNYE	genome polyprotein
44	34	63.0	2292	1 GNNYE	genome polyprotein
45	34	63.0	2292	2 S35961	capsid polyprotein

## ALIGNMENTS

## RESULT 1

I48161  
p-185 precursor - golden hamster  
C:Species: Mesocricetus auratus (golden hamster)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 18-Jun-1999  
C:Accession: I48161  
R:Nakamura, T.; Ushijima, T.; Ishizaka, Y.; Nagao, M.; Arai, M.; Yamazaki, Y.; Ishik.  
Gene 140, 251-255, 1994  
A:Title: Cloning and activation of the Syrian hamster neu proto-oncogene.  
A:Reference number: I48161; MUID:94193007; PMID:7908275  
A:Accession: I48161  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-1254 <RES>  
A:Cross-references: GB:D16295; NID:9493236; PIDN:BAA03801.1; PID:g747595  
C:Genetics:  
A:Gene: neu  
C:Superfamily: epidermal growth factor receptor; protein kinase homology  
C:Keywords: ATP  
F:718-983/Domain: protein kinase homology <KIN>  
F:726-734/Region: protein kinase ATP-binding motif

## Query Match

Best Local Similarity 100.0%; Score 54; DB 2; Length 1254;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EYLVPPQGGF 10

Db 1021 EYLVPPQGGF 1030

## RESULT 2

A24571  
protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - human

N:Alternate names: c-erb-B-2 protein precursor; kinase-related transforming protein e

C:Species: Homo sapiens (man)

C:Date: 25-Oct-1987 #sequence\_revision 06-Dec-1996 #text\_change 11-Jun-1999

C:Accession: A24571; A25491; A44188; B44188; I59509; I57622

R:Yamamoto, T.; Ikawa, S.; Akiyama, T.; Semba, K.; Nomura, N.; Miyajima, N.; Saito, T

Nature 319, 230-234, 1986

A:Title: Similarity of protein encoded by the human c-erb-B-2 gene to epidermal growth

A:Reference number: A24571; MUID:86118663; PMID:3003577

A:Accession: A24571

A:Molecule type: mRNA

A:Residues: 1-1255 <YAM>

A:Cross-references: GB:X03363; NID:g31197; PIDN:CAA27060.1; PID:g31198

R:Semba, K.; Kanata, N.; Toyoshima, K.; Yamamoto, T.

Proc. Natl. Acad. Sci. U.S.A. 82, 6497-6501, 1985

A:Title: A v-erbB-related protooncogene, c-erbB-2, is distinct from the c-erbB-1/epid

A:Reference number: A25491; MUID:86016729; PMID:2995967

A:Accession: A25491

A:Molecule type: DNA

A:Residues: 737-1031 <SEM>  
A:Cross-references: GB:M11767; NID:g182163; PIDN:AAA35808.1; PID:g553282  
R:Coussens, L.; Yang-Feng, T.L.; Liao, Y.C.; Chen, E.; Gray, A.; McGrath, J.; Seeburg, P.  
Science 230, 1132-1139, 1985  
A:Title: Tyrosine kinase receptor with extensive homology to EGF receptor shares chromosomal  
A:Reference number: A44188; MUID:86070181; PMID:2999974  
A:Accession: A44188  
A:Molecule type: DNA  
A:Residues: 740-910 <COU1>  
A:Cross-references: GB:M12036; NID:g183988; PIDN:AAA35978.1; PID:g183989  
A:Accession: B44188  
A:Molecule type: mRNA  
A:Residues: 1-517, 'RALL', 522, 'S', 524-654, 'V', 656-1169, 'A', 1171-1255 <COU2>  
A:Cross-references: GB:M11730; NID:g183986  
R:King, C.R.; Kraus, M.H.; Aaronson, S.A.  
Science 229, 974-976, 1985  
A:Title: Amplification of a novel v-erbB-related gene in a human mammary carcinoma.  
A:Reference number: 159509; MUID:85272597; PMID:2992089  
A:Accession: 159509  
A>Status: translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 832-909 <REX>  
A:Cross-references: GB:L29395; NID:g459807; PIDN:AAA35809.1; PID:g459808  
R:Tal, M.; King, C.R.; Kraus, M.H.; Ullrich, A.; Schlessinger, J.; Givol, D.  
Mol. Cell. Biol. 7, 2597-2601, 1987  
A:Title: Human HER2 (neu) promoter: evidence for multiple mechanisms for transcriptional  
A:Reference number: 157622; MUID:87286898; PMID:3039351  
A:Accession: 157622  
A>Status: translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-191 <TAL>  
A:Cross-references: GB:M16792; NID:g183983; PIDN:AAA58637.1; PID:g553332  
C:Comment: Amplification and overexpression of this erbB-related gene occurs in about 30  
C:Genetics:  
A:Gene: GDB:ERBB2; NGL: NEU; HER-2  
A:Cross-references: GDB:L20613; OMIM:164870  
A:Map position: 17q21.1-17q21.1  
A:Introns: 25/1; 75/3; 147/1; 883/3  
A:Note: the list of introns is incomplete  
C:Function:  
A:Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP  
C:Superfamily: epidermal growth factor receptor; protein kinase homology  
C:Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphoprotein; phospho  
inase  
F:1-21/Domain: signal sequence #status predicted <SIG>  
F:22-1255/Product: protein-tyrosine kinase erbB2 #status predicted <MAT>  
F:22-653/Domain: extracellular #status predicted <EXT>  
F:770-304/Domain: EGF receptor extracellular domain repeat <EE1>  
F:395-605/Domain: EGF receptor extracellular domain repeat <EE2>  
F:654-675/Domain: transmembrane #status predicted <TM>  
F:676-1255/Domain: intracellular #status predicted <INT>  
F:718-983/Domain: protein kinase homology <KIN>  
F:726-734/Region: protein kinase ATP-binding motif  
F:681,124,187,259,530,571,629/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:686/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted  
F:753/Active site: Lys #status predicted  
F:1139,1221,1222,1248/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation)

Query Match 100.08; Score 54; DB 1; Length 1255;  
Best Local Similarity 100.08; Pred. No. 0.033;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYLVPQQGF 10  
|||||  
DB 1021 EBYLVPQQGF 1030

## RESULT 3

TVRTNU

protein-tyrosine kinase (EC 2.7.1.112) neu precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C&gt;Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 11-Jun-1999

C:Accession: A24562; A61204

R:Bargmann, C.I.; Hung, M.C.; Weinberg, R.A.  
Nature 319, 226-230, 1986  
A:Title: The neu oncogene encodes an epidermal growth factor receptor-related protei  
A:Reference number: A24562; MUID:86118662; PMID:3945311  
A:Accession: A24562  
A:Molecule type: mRNA  
A:Residues: 1-1260 <BAR>  
A:Cross-references: EMBL:X03362; NID:g56745; PIDN:CAA27059.1; PID:g56746  
R:Masui, T.; Mann, A.M.; Macatee, T.L.; Garland, E.M.; Okamura, T.; Smith, R.A.; Col  
Carcinogenesis 12, 1975-1978, 1991  
A:Title: Direct DNA sequencing of the rat neu oncogene transmembrane domain reveals  
2-thiazolyl]formamide or N-methyl-N-nitrosourea.  
A:Reference number: A61204; MUID:92035293; PMID:1682063  
A:Accession: A61204  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 637-663, 'V', 665-702 <MAS>  
A:Note: authors translated the codon GCA for residue 25 as Val  
C:Genetics:  
A:Gene: neu  
C:Superfamily: epidermal growth factor receptor; protein kinase homology  
C:Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphoprotein; ph  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-1260/Product: protein-tyrosine kinase neu #status predicted <MAT>  
F:658-680/Domain: transmembrane #status predicted <TM>  
F:723-988/Domain: protein kinase homology <KIN>  
F:731-739/Region: protein kinase ATP-binding motif  
F:711,191,263,535,576,634/Binding site: carbohydrate (Asn) (covalent) #status predic  
F:691/Binding site: phosphate (Thr) (covalent) #status predicted  
F:758/Active site: Lys #status predicted  
F:782,1227,1253/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 100.08; Score 54; DB 1; Length 1260;  
Best Local Similarity 100.08; Pred. No. 0.033;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYLVPQQGF 10  
|||||

DB 1026 EBYLVPQQGF 1035

## RESULT 4

G0HUE

epidermal growth factor receptor precursor - human

N:Contains: protein-tyrosine kinase (EC 2.7.1.112) erbB

C:Species: Homo sapiens (man)

C&gt;Date: 15-Nov-1984 #sequence\_revision 27-Nov-1985 #text\_change 11-Jun-1999

C:Accession: A00641; A25772; S30024; A38672; A00642; A03615; A23062; A05281; A60143

R:Ullrich, A.; Coussens, L.; Hayflick, J.S.; Dull, T.J.; Gray, A.; Tam, A.W.; Lee, R.P.H.  
Nature 309, 418-425, 1984

A:Title: Human epidermal growth factor receptor cDNA sequence and aberrant expressi

A:Reference number: A00641; MUID:84219729; PMID:6328312

A:Accession: A00641

A:Molecule type: mRNA

A:Residues: 1-1210 &lt;ULL&gt;

A:Cross-references: EMBL:X00588; NID:g31113; PIDN:CAA25240.1; PID:g757924  
A:Note: the authors translated the codon AAG for residue 540 as Asn

R:Ishii, S.; Xu, Y.; Stratton, R.H.; Roe, B.A.; Merlino, G.T.; Pastan, I.

Proc. Natl. Acad. Sci. U.S.A. 82, 4920-4924, 1985

A:Title: Characterization and sequence of the promoter region of the human epiderma

A:Reference number: A25772; MUID:85270438; PMID:2991899

A:Accession: A25772

A&gt;Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-29 &lt;ISH&gt;

A:Cross-references: GB:M11234; NID:g181981; PIDN:AAAS2370.1; PID:g553272

R:Haley, J.; Whittle, N.; Bennett, P.; Kinchington, D.; Ullrich, A.; Waterfield, M.

Oncogene Res. 1, 375-396, 1987

A:Title: The human EGF receptor gene: structure of the 110 kb locus and identificat

A:Reference number: S30024; MUID:88217333; PMID:3329716

A:Accession: S30024

A:Molecule type: DNA

A:Residues: 1-29 <HA2>  
A:Cross-references: EMBL:X06370; NID:g31118; PIDN:CAA29668.1; PID:g31119  
R:Haley, J.D.; Waterfield, M.D.  
J. Biol. Chem. 266, 1746-1753, 1991  
A:Title: Contributory effects of de Novo transcription and premature transcript termination  
A:Reference number: A38672; MUID:91107677; PMID:1988448  
A:Accession: A38672  
A:Molecule type: DNA  
A:Residues: 1-29 <HAL>  
A:Cross-references: GB:M38425; NID:g181977; PIDN:AAA63171.1; PID:g553271  
A:Experimental source: carcinoma cell line A431-7  
R:Xu, Y.; Ishii, S.; Clark, A.J.L.; Sullivan, M.; Wilson, R.K.; Ma, D.P.; Roe, B.A.; Merl Nature 309, 806-810, 1984  
A:Title: Human epidermal growth factor receptor cDNA is homologous to a variety of RNAs  
A:Reference number: A00642; MUID:84245835; PMID:6330563  
A:Accession: A00642  
A:Molecule type: mRNA  
A:Residues: 'RCNWRRA', 150-187, 'KSVIQAV', 195, 'M', 197, 'A', 199-222, 'S', 224-304, 'RA', 307-321, '798-799, 'TD', 802-811, 'R', 813-942 <XUY>  
A:Experimental source: A431 human carcinoma cells, which have large numbers of EGF receptor  
R:Lin, C.R.; Chen, W.S.; Krueger, W.; Stolarsky, L.S.; Weber, W.; Evans, R.M.; Verma, I. Science 224, 843-848, 1984  
A:Title: Expression cloning of human EGF receptor complementary DNA: gene amplification  
A:Reference number: A43615; MUID:84196372; PMID:6326261  
A:Accession: A43615  
A:Molecule type: mRNA  
A:Residues: 713-964 <LIN>  
A:Experimental source: epidermoid carcinoma cell line A431  
R:Simmen, F.A.; Gope, M.L.; Schulz, T.Z.; Wright, D.A.; Carpenter, G.; O'Malley, B.W. Biochem. Biophys. Res. Commun. 124, 125-132, 1984  
A:Reference number: A23062; MUID:85046483; PMID:6093780  
A:Accession: A23062  
A:Molecule type: mRNA  
A:Residues: 1028-1210 <STM>  
R:Weber, W.; Gill, G.N.; Speiss, J. Science 224, 294-297, 1984  
A:Reference number: A05281; MUID:84172183; PMID:6324343  
A:Accession: A05281  
A:Molecule type: protein  
A:Residues: 25-30, 'S', 32-51, 454-467 <WEB>  
R:Russo, M.W.; Lukas, T.J.; Cohen, S.; Staros, J.V. J. Biol. Chem. 260, 5205-5208, 1985  
A:Title: Identification of residues in the nucleotide binding site of the epidermal growth factor receptor  
A:Reference number: A60143; MUID:85182650; PMID:2985580  
A:Accession: A60143  
A:Molecule type: protein  
A:Residues: 740-744, 'X', 746-747 <RUS>  
R:Mroczkowski, B.; Mosig, G.; Cohen, S. Nature 309, 270-273, 1984  
A:Title: ATP-stimulated interaction between epidermal growth factor receptor and superoxide dismutase  
A:Reference number: A38023; MUID:84191554; PMID:6325948  
A:Contents: annotation; receptor activity  
A:Note: the EGF receptor (and other tyrosine kinases) can nick double-stranded DNA  
R:Chen, W.S.; Lazar, C.S.; Lund, K.A.; Welsh, J.B.; Chang, C.P.; Walton, G.M.; Der, C.J. Cell 59, 33-43, 1989  
A:Title: Functional independence of the epidermal growth factor receptor from a domain in the EGF ligand  
A:Reference number: A3331; MUID:9003233; PMID:2790960  
A:Contents: annotation; internalization signal  
C:Comment: Binding of EGF to the receptor leads to internalization of the EGF-receptor complex  
C:Genetics:  
A:Gene: GDB:EGFR  
A:Cross-references: GDB:120610; OMIM:131550  
A:Map position: 7p12.3-7p12.1  
C:Superfamily: epidermal growth factor receptor; protein kinase homology  
C:Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphoprotein; phosphotyrosine  
F:1-24/Domain: signal sequence #status predicted <SIG>  
F:25-1210/Product: EGF receptor #status predicted <NAT>  
F:25-645/Domain: extracellular #status predicted <EXT>  
F:75-300/Domain: EGF receptor extracellular domain repeat <EE1>  
F:390-600/Domain: EGF receptor extracellular domain repeat <EE2>  
F:646-668/Domain: transmembrane #status predicted <TM>  
F:669-1210/Domain: intracellular #status predicted <INT>  
F:710-975/Domain: protein kinase homology <KIN>

F:718-726/Region: protein kinase ATP-binding motif  
F:999-1046/Region: coated-pit mediated internalization signal  
F:1047-1210/Region: inhibitory  
F:128, 175, 352, 413, 444, 528, 603/Binding site: carbohydrate (Asn) (covalent) #status p  
F:745/Active site: Lys #status experimental  
Query Match 92.6%; Score 50; DB 1; Length 1210;  
Best Local Similarity 80.0%; Pred. No. 0.19;  
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EBYLPQOGF 10  
DB 1014 DEYLPQOGF 1023  
RESULT 5  
A53183  
epidermal growth factor receptor precursor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 18-Jun-1999  
C:Accession: A53183; A43818; S24942; A28941; S45325; I49643  
R:Luetsteke, N.C.; Phillips, H.K.; Qiu, T.H.; Copeland, N.G.; Earp, H.S.; Jenkins, N. Genes Dev. 8, 399-413, 1994  
A:Title: The mouse waved-2 phenotype results from a point mutation in the EGF receptor  
A:Reference number: A53183; MUID:94170986; PMID:8125255  
A:Accession: A53183  
A:Molecule type: mRNA  
A:Residues: 1-1210 <LUE>  
A:Cross-references: GB:U03425  
R:Avivi, A.; Lax, I.; Ullrich, A.; Schlessinger, J.; Givol, D.; Morse, B. Oncogene 6, 673-676, 1991  
A:Title: Comparison of EGF receptor sequences as a guide to study the ligand binding site  
A:Reference number: A43818; MUID:91232866; PMID:2030916  
A:Accession: A43818  
A:Molecule type: mRNA  
A:Residues: 1-714 <AVI>  
A:Cross-references: GB:X59698  
R:Eisinger, D.P.; Serrero, G. submitted to the EMBL Data Library, June 1992  
A:Reference number: S24942  
A:Accession: S24942  
A:Molecule type: mRNA  
A:Residues: 969-971, 'K', 973-1115, 'D' <EIS>  
A:Cross-references: EMBL:Z12608  
R:Heisermann, G.J.; Gill, G.N. J. Biol. Chem. 263, 13152-13158, 1988  
A:Title: Epidermal growth factor receptor threonine and serine residues phosphorylated by protein kinase C  
A:Reference number: A28941; MUID:88330814; PMID:3138233  
A:Accession: A28941  
A:Molecule type: protein  
A:Residues: 689-694, 'X', 696-704, 'L', 706-707; 989-992, 'XX', 995-996, 'X', 998-1000; 1002-1004, 'X', 1006-1007, 1009-1010, 'X', 1012-1013, 'X', 1015-1016, 'X', 1018-1019, 'X', 1021-1022, 'X', 1024-1025, 'X', 1027-1028, 'X', 1030-1031, 'X', 1033-1034, 'X', 1036-1037, 'X', 1039-1040, 'X', 1042-1043, 'X', 1045-1046, 'X', 1048-1049, 'X', 1051-1052, 'X', 1054-1055, 'X', 1057-1058, 'X', 1060-1061, 'X', 1063-1064, 'X', 1066-1067, 'X', 1069-1070, 'X', 1072-1073, 'X', 1075-1076, 'X', 1078-1079, 'X', 1081-1082, 'X', 1084-1085, 'X', 1087-1088, 'X', 1090-1091, 'X', 1093-1094, 'X', 1096-1097, 'X', 1099-1100, 'X', 1102-1103, 'X', 1105-1106, 'X', 1108-1109, 'X', 1111-1112, 'X', 1114-1115, 'X', 1117-1118, 'X', 1120-1121, 'X', 1123-1124, 'X', 1126-1127, 'X', 1129-1130, 'X', 1132-1133, 'X', 1135-1136, 'X', 1138-1139, 'X', 1141-1142, 'X', 1144-1145, 'X', 1147-1148, 'X', 1150-1151, 'X', 1153-1154, 'X', 1156-1157, 'X', 1159-1160, 'X', 1162-1163, 'X', 1165-1166, 'X', 1168-1169, 'X', 1171-1172, 'X', 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1918-1919, 'X', 1921-1922, 'X', 1924-1925, 'X', 1927-1928, 'X', 1930-1931, 'X', 1933-1934, 'X', 1936-1937, 'X', 1939-1940, 'X', 1942-1943, 'X', 1945-1946, 'X', 1948-1949, 'X', 1951-1952, 'X', 1954-1955, 'X', 1957-1958, 'X', 1960-1961, 'X', 1963-1964, 'X', 1966-1967, 'X', 1969-1970, 'X', 1972-1973, 'X', 1975-1976, 'X', 1978-1979, 'X', 1981-1982, 'X', 1984-1985, 'X', 1987-1988, 'X', 1990-1991, 'X', 1993-1994, 'X', 1996-1997, 'X', 1999-2000, 'X', 2002-2003, 'X', 2005-2006, 'X', 2008-2009, 'X', 2011-2012, 'X', 2014-2015, 'X', 2017-2018, 'X', 2020-2021, 'X', 2023-2024, 'X', 2026-2027, 'X', 2029-2030, 'X', 2032-2033, 'X', 2035-2036, 'X', 2038-2039, 'X', 2041-2042, 'X', 2044-2045, 'X', 2047-2048, 'X', 2050-2051, 'X', 2053-2054, 'X', 2056-2057, 'X', 2059-2060, 'X', 2062-2063, 'X', 2065-2066, 'X', 2068-2069, 'X', 2071-2072, 'X', 2074-2075, 'X', 2077-2078, 'X', 2080-2081, 'X', 2083-2084, 'X', 2086-2087, 'X', 2089-2090, 'X', 2092-2093, 'X', 2095-2096, 'X', 2098-2099, 'X', 2101-2102, 'X', 2104-2105, 'X', 2107-2108, 'X', 2110-2111, 'X', 2113-2114, 'X', 2116-2117, 'X', 2119-2120, 'X', 2122-2123, 'X', 2125-2126, 'X', 2128-2129, 'X', 2131-2132, 'X', 2134-2135, 'X', 2137-2138, 'X', 2140-2141, 'X', 2143-2144, 'X', 2146-2147, 'X', 2149-2150, 'X', 2152-2153, 'X', 2155-2156, 'X', 2158-2159, 'X', 2161-2162, 'X', 2164-2165, 'X', 2167-2168, 'X', 2170-2171, 'X', 2173-2174, 'X', 2176-2177, 'X', 2179-2180, 'X', 2182-2183, 'X', 2185-2186, 'X', 2188-2189, 'X', 2191-2192, 'X', 2194-2195, 'X', 2197-2198, 'X', 2200-2201, 'X', 2203-2204, 'X', 2206-2207, 'X', 2209-2210, 'X', 2212-2213, 'X', 2215-2216, 'X', 2218-2219, 'X', 2221-2222, 'X', 2224-2225, 'X', 2227-2228, 'X', 2230-2231, 'X', 2233-2234, 'X', 2236-2237, 'X', 2239-2240, 'X', 2242-2243, 'X', 2245-2246, 'X', 2248-2249, 'X', 2251-2252, 'X', 2254-2255, 'X', 2257-2258, 'X', 2260-2261, 'X', 2263-2264, 'X', 2266-2267, 'X', 2269-2270, 'X', 2272-2273, 'X', 2275-2276, 'X', 2278-2279, 'X', 2281-2282, 'X', 2284-2285, 'X', 2287-2288, 'X', 2290-2291, 'X', 2293-2294, 'X', 2296-2297, 'X', 2299-2300, 'X', 2302-2303, 'X', 2305-2306, 'X', 2308-2309, 'X', 2311-2312, 'X', 2314-2315, 'X', 2317-2318, 'X', 2320-2321, 'X', 2323-2324, 'X', 2326-2327, 'X', 2329-2330, 'X', 2332-2333, 'X', 2335-2336, 'X', 2338-2339, 'X', 2341-2342, 'X', 2344-2345, 'X', 2347-2348, 'X', 2350-2351, 'X', 2353-2354, 'X', 2356-2357, 'X', 2359-2360, 'X', 2362-2363, 'X', 2365-2366, 'X', 2368-2369, 'X', 2371-2372, 'X', 2374-2375, 'X', 2377-2378, 'X', 2380-2381, 'X', 2383-2384, 'X', 2386-2387, 'X', 2389-2390, 'X', 2392-2393, 'X', 2395-2396, 'X', 2398-2399, 'X', 2401-2402, 'X', 2404-2405, 'X', 2407-2408, 'X', 2410-2411, 'X', 2413-2414, 'X', 2416-2417, 'X', 2419-2420, 'X', 2422-2423, 'X', 2425-2426, 'X', 2428-2429, 'X', 2431-2432, 'X', 2434-2435, 'X', 2437-2438, 'X', 2440-2441, 'X', 2443-2444, 'X', 2446-2447, 'X', 2449-2450, 'X', 2452-2453, 'X', 2455-2456, 'X', 2458-2459, 'X', 2461-2462, 'X', 2464-2465, 'X', 2467-2468, 'X', 2470-2471, 'X', 2473-2474, 'X', 2476-2477, 'X', 2479-2480, 'X', 2482-2483, 'X', 2485-2486, 'X', 2488-2489, 'X', 2491-2492, 'X', 2494-2495, 'X', 2497-2498, 'X', 2500-2501, 'X', 2503-2504, 'X', 2506-2507, 'X', 2509-2510, 'X', 2512-2513, 'X', 2515-2516, 'X', 2518-2519, 'X', 2521-2522, 'X', 2524-2525, 'X', 2527-2528, 'X', 2530-2531, 'X', 2533-2534, 'X', 2536-2537, 'X', 2539-2540, 'X', 2542-2543, 'X', 2545-2546, 'X', 2548-2549, 'X', 2551-2552, 'X', 2554-2555, 'X', 2557-2558, 'X', 2560-2561, 'X', 2563-2564, 'X', 2566-2567, 'X', 2569-2570, 'X', 2572-2573, 'X', 2575-2576, 'X', 2578-2579, 'X', 2581-2582, 'X', 2584-2585, 'X', 2587-2588, 'X', 2590-2591, 'X', 2593-2594, 'X', 2596-2597, 'X', 2599-2600, 'X', 2602-2603, 'X', 2605-2606, 'X', 2608-2609, 'X', 2611-2612, 'X', 2614-2615, 'X', 2617-2618, 'X', 2620-2621, 'X', 2623-2624, 'X', 2626-2627, 'X', 2629-2630, 'X', 2632-2633, 'X', 2635-2636, 'X', 2638-2639, 'X', 2641-2642, 'X', 2644-2645, 'X', 2647-2648, 'X', 2650-2651, 'X', 2653-2654, 'X', 2656-2657, 'X', 2659-2660, 'X', 2662-2663, 'X', 2665-2666, 'X', 2668-2669, 'X', 2671-2672, 'X', 2674-2675, 'X', 2677-2678, 'X', 2680-2681, 'X', 2683-2684, 'X', 2686-2687, 'X', 2689-2690, 'X', 2692-2693, 'X', 2695-2696, 'X', 2698-2699, 'X', 2701-2702, 'X', 2704-2705, 'X', 2707-2708, 'X', 2710-2711, 'X', 2713-2714, 'X', 2716-2717, 'X', 2719-2720, 'X', 2722-2723, 'X', 2725-2726, 'X', 2728-2729, 'X', 2732-2733, 'X', 2735-2736, 'X', 2738-2739, 'X', 2741-2742, 'X', 2744-2745, 'X', 2747-2748, 'X', 2750-2751, 'X', 2753-2754, 'X', 2756-2757, 'X', 2759-2760, 'X', 2762-2763, 'X', 2765-2766, 'X', 2768-2769, 'X', 2771-2772, 'X', 2774-2775, 'X', 2777-2778, 'X', 2780-2781, 'X', 2783-2784, 'X', 2786-2787, 'X', 2789-2790, 'X', 2792-2793, 'X', 2795-2796, 'X', 2798-2799, 'X', 2801-2802, 'X', 2804-2805, 'X', 2807-2808, 'X', 2810-2811, 'X', 2813-2814, 'X', 2816-2817, 'X', 2819-2820, 'X', 2822-2823, 'X', 2825-2826, 'X', 2828-2829, 'X', 2831-2832, 'X', 2834-2835, 'X', 2837-2838, 'X', 2840-2841, 'X', 2843-2844, 'X', 2846-2847, 'X', 2849-2850, 'X', 2852-2853, 'X', 2855-2856, 'X', 2858-2859, 'X', 2861-2862, 'X', 2864-2865, 'X', 2867-2868, 'X', 2870-2871, 'X', 2873-2874, 'X', 2876-2877, 'X', 2879-2880, 'X', 2882-2883, 'X', 2885-2886, 'X', 2888-2889, 'X', 2891-2892, 'X', 2894-2895, 'X', 2897-2898, 'X', 2900-2901, 'X', 2903-2904, 'X', 2906-2907, 'X', 2909-2910, 'X', 2912-2913, 'X', 2915-2916, 'X', 2918-2919, 'X', 2921-2922, 'X', 2924-2925, 'X', 2927-2928, 'X', 2930-2931, 'X', 2933-2934, 'X', 2936-2937, 'X', 2939-2940, 'X', 2942-2943, 'X', 2945-2946, 'X', 2948-2949, 'X', 2951-2952, 'X', 2954-2955, 'X', 2957-2958, 'X', 2960-2961, 'X', 2963-2964, 'X', 2966-2967, 'X', 2969-2970, 'X', 2972-2973, 'X', 2975-2976, 'X', 2978-2979, 'X', 2981-2982, 'X', 2984-2985, 'X', 2987-2988, 'X', 2990-2991, 'X', 2993-2994, 'X', 2996-2997,

F:1-24/Domain: signal sequence #status predicted <SIG>  
 F:648-670/Domain: transmembrane #status predicted <TM>  
 F:712-977/Domain: protein kinase homology <KIN>  
 F:720-728/Region: protein kinase ATP-binding motif  
 F:680-695/Binding site: phosphate (Thr) (covalent) #status experimental  
 F:697,1070,1071/Binding site: phosphate (Ser) (covalent) #status experimental  
 F:993/Binding site: (or 997) phosphate (Ser) (covalent) #status experimental  
 F:1028/Binding site: (or 1030 or 1032) phosphate (Ser) (covalent) #status experimental  
 F:1197/Binding site: phosphate (Tyr) (covalent) #status experimental

Query Match 92.6%; Score 50; DB 2; Length 1210;  
 Best Local Similarity 80.0%; Pred. No. 0.19;  
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEYLVPOQGF 10  
 :|||||  
 Db 1016 DEYLVPHQGF 1025

## RESULT 6

TVFVB

protein-tyrosine kinase (EC 2.7.1.112) erbB - avian erythroblastosis virus (strain ES4)  
 C:Species: avian erythroblastosis virus  
 C>Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 11-Jun-1999

C:Accession: A25231; B25231  
 R:Choi, O.R.; Trainor, C.; Graf, T.; Beug, H.; Engel, J.D.

Mol. Cell. Biol. 6, 1751-1759, 1986  
 A:Title: A single amino acid substitution in v-erbB confers a thermolabile phenotype to

A:Reference number: A25231; MUID:87064458; PMID:2878364  
 A:Accession: A25231  
 A:Molecule type: DNA

A:Residues: 1-540 <CHO>  
 A:Cross-references: GB:M13179; NID:q209679; PIDN:AAA42401.1; PID:q209680

A:Note: the authors translated the codon AAG for residue 157 as Gly, ATG for residue 253  
 C:Genetics:  
 A:Gene: erbB

C:Superfamily: epidermal growth factor receptor; protein kinase homology  
 C:Keywords: ATP; oncogene; phosphotransferase; transforming protein; tyrosine-specific  
 F:130-395/Domain: protein kinase homology <KIN>  
 F:138-146/Region: protein kinase ATP-binding motif  
 F:165/Active site: Lys #status predicted

Query Match 85.2%; Score 46; DB 1; Length 540;  
 Best Local Similarity 80.0%; Pred. No. 0.48;  
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEYLVPOQGF 10  
 :|||||  
 Db 434 DEYLVPHQGF 443

## RESULT 7

B44776

protein-tyrosine kinase (EC 2.7.1.112) erbB - avian erythroblastosis virus (strain ES4)  
 C:Species: avian erythroblastosis virus  
 C>Date: 28-Apr-1993 #sequence\_revision 28-Apr-1993 #text\_change 04-Feb-2000

C:Accession: B44776  
 R:Bruskin, A.; Jackson, J.; Bishop, J.M.; McCarley, D.J.; Schatzman, R.C.

Oncogene 5, 15-24, 1990  
 A:Title: Six amino acids from the retroviral gene gag greatly enhance the transforming

A:Reference number: A44776; MUID:90206603; PMID:1969616  
 A:Accession: B44776  
 A:Status: preliminary

A:Molecule type: mRNA  
 A:Residues: 1-540 <BRD>

A:Cross-references: GB:X52211  
 C:Genetics:

A:Gene: erbB  
 C:Superfamily: epidermal growth factor receptor; protein kinase homology

C:Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase  
 F:130-395/Domain: protein kinase homology <KIN>

F:138-146/Region: protein kinase ATP-binding motif  
 F:165/Active site: Lys #status predicted

Query Match 85.2%; Score 46; DB 2; Length 540;  
 Best Local Similarity 80.0%; Pred. No. 0.48;  
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEYLVPOQGF 10  
 :|||||  
 Db 434 DEYLVPHQGF 443

## RESULT 8

S35745

protein-tyrosine kinase (EC 2.7.1.112) erbB - avian erythroblastosis virus  
 C:Species: avian erythroblastosis virus  
 C>Date: 03-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 28-Feb-1997

C:Accession: S35745  
 R:Vennstroem, B.

submitted to the EMBL Data Library, March 1993  
 A:Reference number: S35743

A:Accession: S35745  
 A:Molecule type: DNA

A:Residues: 1-544 <VEN>  
 A:Cross-references: EMBL:X12707

C:Genetics:  
 A:Gene: erbB

C:Superfamily: epidermal growth factor receptor; protein kinase homology  
 C:Keywords: ATP; oncogene; phosphotransferase; transforming protein; tyrosine-specific  
 F:135-400/Domain: protein kinase homology <KIN>  
 F:143-151/Region: protein kinase ATP-binding motif  
 F:170/Active site: Lys #status predicted

Query Match 85.2%; Score 46; DB 2; Length 544;  
 Best Local Similarity 80.0%; Pred. No. 0.49;  
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEYLVPOQGF 10  
 :|||||  
 Db 439 DEYLVPHQGF 448

## RESULT 9

S00727

kinase-related transforming protein (erbB) (EC 2.7.1.-) - avian erythroblastosis virus  
 C:Species: avian erythroblastosis virus  
 C>Date: 01-Dec-1989 #sequence\_revision 01-Dec-1989 #text\_change 28-Feb-1997

C:Accession: S00727  
 R:Scotting, P.; Vennstrom, B.; Jansen, M.; Graf, T.; Beug, H.; Hayman, M.J.

Oncogene Res. 1, 265-278, 1987  
 A:Title: Common site of mutation in the erbB gene of avian erythroblastosis virus mut

A:Reference number: S00727; MUID:88217326; PMID:2897102  
 A:Accession: S00727  
 A:Molecule type: DNA

A:Residues: 1-545 <SCO>  
 A:Cross-references: EMBL:X06943

C:Genetics:  
 A:Gene: erbB

C:Superfamily: epidermal growth factor receptor; protein kinase homology  
 C:Keywords: ATP; phosphotransferase  
 F:135-400/Domain: protein kinase homology <KIN>  
 F:143-151/Region: protein kinase ATP-binding motif

Query Match 85.2%; Score 46; DB 2; Length 545;  
 Best Local Similarity 80.0%; Pred. No. 0.49;  
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEYLVPOQGF 10  
 :|||||  
 Db 439 DEYLVPHQGF 448

## RESULT 10

TVFVB

protein-tyrosine kinase (EC 2.7.1.112) erbB - avian erythroblastosis virus (strain H)  
 C:Species: avian erythroblastosis virus

C;Date: 18-Apr-1984 #sequence\_revision 18-Apr-1984 #text\_change 11-Jun-1999  
 C;Accession: A00644; A38022  
 R;Yamamoto, T.; Nishida, T.; Miyajima, N.; Kawai, S.; Ooi, T.; Toyoshima, K.  
 Cell 35, 71-78, 1983  
 A;Title: The erbB gene of avian erythroblastosis virus is a member of the src gene family  
 A;Reference number: A00644; MUID:84026539; PMID:6313229  
 A;Accession: A00644  
 A;Molecule type: DNA  
 A;Residues: 1-604 <YAM>  
 A;Cross-references: GB:K01216; NID:g209676; PIDN:AAA2400.1; PID:g209678  
 R;Debulre, B.; Henry, C.; Benalissa, M.; Biserte, G.; Claverie, J.M.; Saule, S.; Martin, S.  
 Science 244, 1456-1459, 1984  
 A;Title: Sequencing the erbA gene of avian erythroblastosis virus reveals a new type of  
 A;Reference number: A38022; MUID:84223957; PMID:6328658  
 A;Accession: A38022  
 A;Molecule type: DNA  
 A;Residues: 1-28, 'W', 30-139, 'F', 141-145, 'V', 147-152 <DEB>  
 A;Cross-references: GB:K02006  
 C;Genetics: erbB  
 C;Superfamily: epidermal growth factor receptor; protein kinase homology  
 C;Keywords: ATP; oncogene; phosphotransferase; transforming protein; tyrosine-specific P  
 F:130-395/Domain: protein kinase homology <KIN>  
 F:138-146/Region: protein kinase ATP-binding motif  
 F:165/Active site: Lys #status predicted

Query Match 85.2%; Score 46; DB 1; Length 604;  
 Best Local Similarity 80.0%; Pred. No. 0.55;  
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 EEYLVPOQGF 10  
 :||||| |||  
 Db 434 DEYLVPHQGF 443  
 :||||| |||  
 RESULT 11  
 TVFVLV  
 N;Contains: protein-tyrosine kinase (EC 2.7.1.112) erbB - avian leukosis virus  
 C;Species: avian leukosis virus, ALV  
 C;Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 11-Jun-1999  
 C;Accession: B00643; A00643  
 R;Nilsen, T.W.; Maroney, P.A.; Goodwin, R.G.; Rottman, F.M.; Crittenden, L.B.; Raines, M.  
 Cell 41, 719-726, 1985  
 A;Title: c-erbB activation in ALV-induced erythroblastosis: novel RNA processing and pro  
 A;Reference number: A00643; MUID:85228222; PMID:2988784  
 A;Accession: B00643  
 A;Molecule type: mRNA  
 A;Residues: 1-698 <NIL>  
 A;Cross-references: GB:M13881; NID:g211749; PIDN:AAA48763.1; PID:g211750  
 A;Note: in Genbank entry CHKERBFF, release 109.0, the source is designated as Gallus gal  
 C;Comment: This protein is synthesized as a gag-env-erbB protein.  
 C;Genetics: erbB  
 A;Gene: gag-env-erbB  
 C;Superfamily: epidermal growth factor receptor; protein kinase homology  
 C;Keywords: ATP; oncogene; phosphotransferase; transforming protein; tyrosine-specific P  
 F:1-6/Product: gag protein (fragment) #status predicted <GAG>  
 F:7-59/Product: env protein (fragment) #status predicted <ENV>  
 F:60-698/Product: protein-tyrosine kinase erbB #status predicted <ERB>  
 F:194-459/Domain: protein-tyrosine kinase homology <KIN>  
 F:202-210/Region: protein kinase ATP-binding motif  
 F:229/Active site: Lys #status predicted

Query Match 85.2%; Score 46; DB 1; Length 698;  
 Best Local Similarity 80.0%; Pred. No. 0.64;  
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 EEYLVPOQGF 10  
 :||||| |||  
 Db 498 DEYLVPHQGF 507  
 :||||| |||  
 RESULT 12

TVCHLV  
 N;Contains: protein-tyrosine kinase (EC 2.7.1.112) erbB  
 C;Species: Gallus gallus (chicken)  
 C;Date: 28-Feb-1986 #sequence\_revision 05-May-1995 #text\_change 04-Feb-2000  
 C;Accession: A27720; A00643  
 R;Lax, I.; Johnson, A.; Howk, R.; Sap, J.; Bellot, F.; Winkler, M.; Ullrich, A.; Ven  
 Mol. Cell. Biol. 8, 1970-1978, 1988  
 A;Title: Chicken epidermal growth factor (EGF) receptor: cDNA cloning, expression in  
 A;Reference number: A27720; MUID:86261272; PMID:3260329  
 A;Accession: A27720  
 A;Molecule type: mRNA  
 A;Residues: 1-1223 <LAX>  
 A;Cross-references: GB:M20386  
 R;Nilsen, T.W.; Maroney, P.A.; Goodwin, R.G.; Rottman, F.M.; Crittenden, L.B.; Raines  
 Cell 41, 719-726, 1985  
 A;Title: c-erbB activation in ALV-induced erythroblastosis: novel RNA processing and  
 A;Reference number: A00643; MUID:85228222; PMID:2988784  
 A;Accession: A00643  
 A;Molecule type: mRNA  
 A;Residues: 585-1223 <NIL>  
 A;Cross-references: GB:M10066  
 C;Genetics: erbB  
 C;Superfamily: epidermal growth factor receptor; protein kinase homology  
 C;Keywords: alternative splicing; ATP; autophosphorylation; glycoprotein; growth fac  
 F:1-30/Domain: signal sequence #status predicted <SIG>  
 F:31-1223/Product: epidermal growth factor receptor #status predicted <MAT>  
 F:31-654/Domain: extracellular #status predicted <EXT>  
 F:81-307/Domain: EGF receptor extracellular domain repeat <EEL>  
 F:397-610/Domain: EGF receptor extracellular domain repeat <EE2>  
 F:655-677/Domain: EGF receptor extracellular domain repeat <EEL>  
 F:678-1223/Domain: transmembrane #status predicted <TMW>  
 F:719-984/Domain: intracellular #status predicted <INT>  
 F:727-735/Region: protein kinase homology <KIN>  
 F:136,202,280,361,370,422,575,580,615,635/Binding site: carbohydrate (Thr) (covalent);  
 F:192,650/Binding site: carbohydrate (Ser) (covalent) #status predicted  
 F:687/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted  
 F:754/Active site: Lys #status predicted  
 F:1100,1183,1208/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #  
 Query Match 85.2%; Score 46; DB 1; Length 1223;  
 Best Local Similarity 80.0%; Pred. No. 1.2;  
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 EEYLVPOQGF 10  
 :||||| |||  
 Db 1023 DEYLVPHQGF 1032  
 :||||| |||  
 RESULT 13  
 S77110  
 hypothetical protein sl11773 - Synecchocystis sp. (strain PCC 6803)  
 C;Species: Synecchocystis sp.  
 A;Variety: PCC 6803  
 C;Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 20-Jun-2000  
 C;Accession: S77110  
 R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima,  
 O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas  
 DNA Res. 3, 109-136, 1996  
 A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecchocys  
 S.  
 A;Reference number: S74322; MUID:97061201; PMID:8905231  
 A;Accession: S77110  
 A;Status: nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-232 <KAN>  
 A;Cross-references: EMBL:D90908; GB:AB001339; NID:g1652725; PIDN:BAAL1768.1; PID:g165  
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996  
 C;Superfamily: conserved hypothetical protein sl11773  
 Query Match 70.4%; Score 38; DB 2; Length 232;

Best Local Similarity 60.0%; Pred. No. 7.1;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EYLVPOQGF 10  
|:|:|  
Db 45 EDYAPQGF 54

## RESULT 14

S68092

protein-glutamine gamma-glutamyltransferase (EC 2.3.2.13) 2, splice form 3 - human

C:Species: Homo sapiens (man)  
C:Date: 21-Apr-1997 #sequence\_revision 09-May-1997 #text\_change 05-May-2000  
C:Accession: S68092  
R:Fraaij, B.M.; Gonzales, R.A.  
Biochim. Biophys. Acta 1306, 63-74, 1996  
A:Title: A third human tissue transglutaminase homologue as a result of alternative gene  
A:Reference number: S68092; MUID:96201707; PMID:8611626  
A:Accession: S68092  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-349 <FRA>

A:Cross-references: GB:S81734; NID:g1478006; PIDN:AAB36379.1; PID:g1478007

C:Genetics:

A:Gene: GDB:TGM2

A:Cross-references: GDB:128013; OMIM:190196

A:Map position: 20q11.2-20q12

C:Keywords: alternative splicing; aminoacyltransferase

Query Match 68.5%; Score 37; DB 2; Length 349;  
Best Local Similarity 60.0%; Pred. No. 18;

Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EYLVPOQGF 10  
|:|:|  
Db 157 QEYVLTQGF 166

## RESULT 15

AE1611

probable proteinase homolog lin1430 [imported] - Listeria innocua (strain Clip11262)

C:Species: Listeria innocua  
C:Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 17-May-2002  
C:Accession: AE1611  
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker  
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.  
D.; Jones, L.M.; Karst, U.  
Science 294, 849-852, 2001  
A:Authors: Kref, J.; Kuhn, M.; Kunst, F.; Kurapk, G.; Madueno, E.; Maitournam, A.; Ma  
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlund,  
A:Title: Comparative genomics of Listeria species.  
A:Reference number: AE1077; MUID:21537279; PMID:11679669

A:Accession: AE1611

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-428 <GLA>

A:Cross-references: GB:AL592022; PIDN:CAC96661.1; PID:g16413903; GSPDB:GN00178

A:Experimental source: strain Clip11262

C:Genetics:

A:Gene: lin1430

C:Superfamily: mitochondrial processing peptidase alpha chain

Query Match 68.5%; Score 37; DB 2; Length 428;

Best Local Similarity 75.0%; Pred. No. 22;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 YLVPOQGF 10  
|:|:|  
Db 25 YLLPKQGF 32

Search completed: July 28, 2003, 17:06:43  
Job time : 42 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 28, 2003, 17:06:05 ; Search time 50 seconds  
(without alignments)  
23.752 Million cell updates/sec

Title: US-09-930-125-3  
Perfect score: 54  
Sequence: 1 EBYLVPQGGF 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 451899 seqs, 118759770 residues

Total number of hits satisfying chosen parameters: 451899

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA:

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2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/2/pubpaa/US09C\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10C\_NEW\_PUB.pep.\*  
17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	10	10	US-09-930-125-3
2	54	100.0	59	10	US-09-854-356-5
3	54	100.0	266	10	US-09-854-356-4
4	54	100.0	293	15	US-10-102-806-583
5	54	100.0	583	10	US-09-930-125-8
6	54	100.0	587	10	US-09-930-125-10
7	54	100.0	589	10	US-09-930-125-11
8	54	100.0	600	10	US-09-854-356-7
9	54	100.0	712	10	US-09-854-356-6
10	54	100.0	919	10	US-10-146-473-72
11	54	100.0	1253	15	US-09-811-123-9
12	54	100.0	1255	9	US-09-811-115-3
13	54	100.0	1255	9	US-09-769-508-2
14	54	100.0	1255	10	US-09-854-356-1
15	54	100.0	1255	10	US-09-854-356-1

16	54	100.0	1255	10	US-09-930-125-2	Sequence 2, Appli
17	54	100.0	1255	11	US-09-441-411-6	Sequence 6, Appli
18	54	100.0	1255	15	US-10-207-655-45	Sequence 45, Appl
19	54	100.0	1255	15	US-10-177-293-126	Sequence 126, App
20	54	100.0	1256	10	US-09-854-356-2	Sequence 2, Appli
21	54	100.0	1256	10	US-09-854-356-14	Sequence 14, Appl
22	54	100.0	1260	10	US-09-870-759-118	Sequence 118, Appl
23	50	92.6	1210	9	US-09-725-433-2	Sequence 2, Appli
24	43	79.6	73	10	US-09-796-692-1649	Sequence 1649, Ap
25	43	79.6	73	10	US-09-796-692-2500	Sequence 2500, Ap
26	43	79.6	73	15	US-10-040-862-1649	Sequence 1649, Ap
27	43	79.6	73	15	US-10-040-862-2500	Sequence 2500, Ap
28	43	79.6	115	9	US-09-925-302-708	Sequence 708, App
29	37	68.5	687	14	US-10-029-654-10	Sequence 10, Appl
30	37	68.5	705	11	US-09-158-722-4	Sequence 4, Appli
31	37	68.5	1308	10	US-09-940-101-2	Sequence 2, Appli
32	37	68.5	1308	15	US-10-207-655-47	Sequence 47, Appl
33	36	66.7	461	9	US-09-925-299-957	Sequence 957, App
34	36	66.7	461	11	US-09-925-299-957	Sequence 957, App
35	36	66.7	461	15	US-10-106-698-5254	Sequence 5254, Ap
36	36	66.7	497	15	US-10-156-761-8691	Sequence 8691, Ap
37	34	63.0	30	9	US-09-864-761-46868	Sequence 46868, A
38	34	63.0	262	9	US-09-815-242-11607	Sequence 11607, A
39	33	61.1	72	9	US-09-864-761-41671	Sequence 41671, A
40	33	61.1	148	9	US-09-864-761-37790	Sequence 37790, A
41	33	61.1	219	15	US-10-156-761-9655	Sequence 9655, A
42	33	61.1	523	10	US-09-910-174A-11	Sequence 11, Appl
43	33	61.1	523	10	US-09-955-866-10	Sequence 10, Appl
44	33	61.1	523	10	US-09-896-738-16	Sequence 16, Appl
45	33	61.1	527	10	US-09-910-174A-10	Sequence 10, Appl

## ALIGNMENTS

## RESULT 1

US-09-930-125-3  
; Sequence 3, Application US/09930125  
; Publication No. US20020193329A1  
; GENERAL INFORMATION:  
; APPLICANT: Hand-Zimmerman, Susan  
; APPLICANT: Cheever, Martin A.  
; APPLICANT: Foy, Teresa M.  
; APPLICANT: Lodes, Michael J.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Vedvick, Thomas S.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS  
; FILE REFERENCE: 210121.544  
; CURRENT APPLICATION NUMBER: US/09/930,125  
; CURRENT FILING DATE: 2001-08-14  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 3  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-930-125-3

Query Match 100.0%; Score 54; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.00036;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EBYLVPQGGF 10  
|||||

Db 1 EBYLVPQGGF 10

## RESULT 2

US-09-854-356-5  
; Sequence 5, Application US/09854356  
; Patent No. US2002017567A1

```
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Gheysen, Dirk
; APPLICANT: Corixa Corporation
; APPLICANT: Smithkline Beecham Biologicals S. A.
; TITLE OF INVENTION: HER-2/neu Fusion Proteins
; FILE REFERENCE: 014058-009810PC
; CURRENT APPLICATION NUMBER: US/09/854,356
; CURRENT FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: US 09/493,480
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,976
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: fragment of the phosphorylation domain, preferred
; OTHER INFORMATION: portion (delta PD) of human HER-2/neu
US-09-854-356-5

Query Match      100.0%; Score 54; DB 10; Length 59;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EEYLVPOQGF 10
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DB      32 EEYLVPOQGF 41

RESULT 3
US-09-854-356-4
; Sequence 4, Application US/09854356
; Patent No. US20020177567A1
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Gheysen, Dirk
; APPLICANT: Corixa Corporation
; APPLICANT: Smithkline Beecham Biologicals S. A.
; TITLE OF INVENTION: HER-2/neu Fusion Proteins
; FILE REFERENCE: 014058-009810PC
; CURRENT APPLICATION NUMBER: US/09/854,356
; CURRENT FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: US 09/493,480
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,976
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: phosphorylation domain (PD) of human HER-2/neu
US-09-854-356-4

Query Match      100.0%; Score 54; DB 10; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EEYLVPOQGF 10
        |||||
DB      32 EEYLVPOQGF 41

RESULT 4
US-10-102-806-583
; Sequence 583, Application US/10102806
; Publication No. US20030054421A1
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DP? or 102(b)?

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; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA103P1C1
; CURRENT APPLICATION NUMBER: US/10/102,806
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 09/925,298
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 583
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (52)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (53)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (58)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (150)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (171)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (207)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (254)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-102-806-583

Query Match      100.0%; Score 54; DB 15; Length 293;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EEYLVPOQGF 10
        |||||
DB      105 EEYLVPOQGF 114

RESULT 5
US-09-930-125-9
; Sequence 9, Application US/09930125
; Publication No. US20020193329A1
; GENERAL INFORMATION:
; APPLICANT: Hand-Zimmerman, Susan
; APPLICANT: Cheever, Martin A.
; APPLICANT: Foy, Teresa M.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Vedvick, Thomas S.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.544
; CURRENT APPLICATION NUMBER: US/09/930,125
; CURRENT FILING DATE: 2001-08-14
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 583
; TYPE: PRT
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; ORGANISM: Homo sapiens  
US-09-930-125-9

Query Match 100.0%; Score 54; DB 10; Length 583;  
Best Local Similarity 100.0%; Pred. No. 0.03;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EYLVPOQGF 10  
Db 347 EYLVPOQGF 356

RESULT 6

US-09-930-125-8  
; Sequence 8, Application US/09930125  
; Publication No. US20020193329A1

; GENERAL INFORMATION:

; APPLICANT: Hand-Zimmerman, Susan

; APPLICANT: Cheever, Martin A.

; APPLICANT: Foy, Teresa M.

; APPLICANT: Lodes, Michael J.

; APPLICANT: Kalos, Michael D.

; APPLICANT: McNeill, Patricia D.

; APPLICANT: Vedvick, Thomas S.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS

; FILE REFERENCE: 210121.544

; CURRENT APPLICATION NUMBER: US/09/930,125

; CURRENT FILING DATE: 2001-08-14

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 8

; LENGTH: 587

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-930-125-8

Query Match 100.0%; Score 54; DB 10; Length 587;  
Best Local Similarity 100.0%; Pred. No. 0.03;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EYLVPOQGF 10  
Db 347 EYLVPOQGF 356

RESULT 7

US-09-930-125-10  
; Sequence 10, Application US/09930125  
; Publication No. US20020193329A1

; GENERAL INFORMATION:

; APPLICANT: Hand-Zimmerman, Susan

; APPLICANT: Cheever, Martin A.

; APPLICANT: Foy, Teresa M.

; APPLICANT: Lodes, Michael J.

; APPLICANT: Kalos, Michael D.

; APPLICANT: McNeill, Patricia D.

; APPLICANT: Vedvick, Thomas S.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS

; FILE REFERENCE: 210121.544

; CURRENT APPLICATION NUMBER: US/09/930,125

; CURRENT FILING DATE: 2001-08-14

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 10

; LENGTH: 589

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-930-125-10

Query Match 100.0%; Score 54; DB 10; Length 589;  
Best Local Similarity 100.0%; Pred. No. 0.03;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 EYLVPOQGF 10  
Db 355 EYLVPOQGF 364

RESULT 8

US-09-930-125-11

; Sequence 11, Application US/09930125

; Publication No. US20020193329A1

; GENERAL INFORMATION:

; APPLICANT: Hand-Zimmerman, Susan

; APPLICANT: Cheever, Martin A.

; APPLICANT: Foy, Teresa M.

; APPLICANT: Lodes, Michael J.

; APPLICANT: Kalos, Michael D.

; APPLICANT: McNeill, Patricia D.

; APPLICANT: Vedvick, Thomas S.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS

; FILE REFERENCE: 210121.544

; CURRENT APPLICATION NUMBER: US/09/930,125

; CURRENT FILING DATE: 2001-08-14

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 11

; LENGTH: 600

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-930-125-11

Query Match 100.0%; Score 54; DB 10; Length 600;  
Best Local Similarity 100.0%; Pred. No. 0.03;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EYLVPOQGF 10  
Db 366 EYLVPOQGF 375

RESULT 9

US-09-854-356-7

; Sequence 7, Application US/09854356

; Patent No. US20020177567A1

; GENERAL INFORMATION:

; APPLICANT: Cheever, Martin A.

; APPLICANT: Gheysen, Dirk

; APPLICANT: Corixa Corporation

; APPLICANT: SmithKline Beecham Biologicals S. A.

; TITLE OF INVENTION: HER-2/neu Fusion Proteins

; FILE REFERENCE: 014058-009810P

; CURRENT APPLICATION NUMBER: US/09/854,356

; CURRENT FILING DATE: 2001-05-09

; PRIOR APPLICATION NUMBER: US 09/293,480

; PRIOR FILING DATE: 2000-01-28

; PRIOR APPLICATION NUMBER: US 60/117,976

; PRIOR FILING DATE: 1999-01-29

; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: PatentIn ver. 2.1

; SEQ ID NO 7

; LENGTH: 712

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: fusion protein  
; OTHER INFORMATION: of ECD and delta PD of human HER-2/neu

Query Match

Best Local Similarity

Matches

10; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

Qy 1 EEYLVPOQGF 10  
|  
Db 685 EEYLVPOQGF 694

RESULT 10  
US-09-854-356-6  
; Sequence 6, Application US/09854356  
; Patent No. US20020177567A1  
; GENERAL INFORMATION:  
; APPLICANT: Cheevers, Martin A.  
; APPLICANT: Cheysen, Dirk  
; APPLICANT: Corixa Corporation  
; APPLICANT: SmithKline Beecham Biologicals S. A.  
; TITLE OF INVENTION: HER-2/neu Fusion Proteins  
; FILE REFERENCE: 014058-009810PC  
; CURRENT APPLICATION NUMBER: US/09/854,356  
; CURRENT FILING DATE: 2001-05-09  
; PRIOR APPLICATION NUMBER: US/09/493,480  
; PRIOR FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: US/09/117,976  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 919  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: fusion protein  
; OTHER INFORMATION: of ECD and PD of human HER-2/neu  
US-09-854-356-6

Query Match 100.0%; Score 54; DB 10; Length 919;  
Best Local Similarity 100.0%; Pred. No. 0.048;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEYLVPOQGF 10  
|  
Db 685 EEYLVPOQGF 694

RESULT 11  
US-10-146-473-72  
; Sequence 72, Application US/10146473  
; Publication No. US2003010888A1  
; GENERAL INFORMATION:  
; APPLICANT: Scanlan, Matthew  
; APPLICANT: Gout, Ivan  
; APPLICANT: Stockert, Elisabeth  
; APPLICANT: Gure, Ali  
; APPLICANT: Chen, Yao-Tseng  
; APPLICANT: Old, Lloyd  
; TITLE OF INVENTION: Breast Cancer Antigens  
; FILE REFERENCE: L00461/70130(JRV)  
; CURRENT APPLICATION NUMBER: US/10/146,473  
; CURRENT FILING DATE: 2002-05-15  
; PRIOR APPLICATION NUMBER: US/09/291,150  
; PRIOR FILING DATE: 2001-05-15  
; NUMBER OF SEQ ID NOS: 82  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 72  
; LENGTH: 1253  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-146-473-72

Query Match 100.0%; Score 54; DB 15; Length 1253;  
Best Local Similarity 100.0%; Pred. No. 0.068;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEYLVPOQGF 10  
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Db 685 EEYLVPOQGF 694

Db 1021 EEYLVPOQGF 1030

RESULT 12  
US-09-811-123-9  
; Sequence 9, Application US/09811123  
; Patent No. US2002001587A1  
; GENERAL INFORMATION:  
; APPLICANT: Sharon Erickson  
; APPLICANT: Ralph Schwall  
; APPLICANT: Mark Sliwkowski  
; TITLE OF INVENTION: METHODS OF TREATMENT USING ANTI-ErbB  
; FILE REFERENCE: GENENT.073A2  
; CURRENT APPLICATION NUMBER: US/09/811,123  
; CURRENT FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/238,327  
; PRIOR FILING DATE: 2000-10-05  
; PRIOR APPLICATION NUMBER: 09/602,530  
; PRIOR FILING DATE: 2000-06-23  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 1255  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-811-123-9

Query Match 100.0%; Score 54; DB 9; Length 1255;  
Best Local Similarity 100.0%; Pred. No. 0.068;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEYLVPOQGF 10  
|  
Db 1021 EEYLVPOQGF 1030

RESULT 13  
US-09-811-115-3  
; Sequence 3, Application US/09811115  
; Patent No. US20020035736A1  
; GENERAL INFORMATION:  
; APPLICANT: Erickson, Sharon  
; APPLICANT: Schwall, Ralph  
; APPLICANT: King, Kathleen  
; TITLE OF INVENTION: HER-2 TRANSGENIC NON-HUMAN TUMOR MODEL  
; FILE REFERENCE: GENENT.034A  
; CURRENT APPLICATION NUMBER: US/09/811,115  
; CURRENT FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/189,844  
; PRIOR FILING DATE: 2000-03-16  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 1255  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-811-115-3

Query Match 100.0%; Score 54; DB 9; Length 1255;  
Best Local Similarity 100.0%; Pred. No. 0.068;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEYLVPOQGF 10  
|  
Db 1021 EEYLVPOQGF 1030

RESULT 14  
US-09-769-508-2  
; Sequence 2, Application US/09769508  
; Patent No. US2002015527A1  
; GENERAL INFORMATION:

APPLICANT: STUART, SUSAN G.  
APPLICANT: MONAHAN, JOHN J.  
APPLICANT: LANGTON, BEATRICE CLAUDIA  
APPLICANT: HANCOCK, MIRIAM E.C.  
APPLICANT: CHAO, LORRINE A.  
APPLICANT: BLUFORD, PETER  
TITLE OF INVENTION: C-ERBB-2 EXTERNAL DOMAIN: GP75  
FILE REFERENCE: BEBIO-111-C1  
CURRENT APPLICATION NUMBER: US/09/769,508  
CURRENT FILING DATE: 2001-01-26  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 1255  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-769-508-2

Query Match 100.0%; Score 54; DB 10; Length 1255;  
Best Local Similarity 100.0%; Pred. No. 0.068;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EYLVPPQGF 10  
Db 1021 EYLVPPQGF 1030

RESULT 15  
US-09-854-356-1  
Sequence 1, Application US/09854356  
Patent No. US20020177567A1  
GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
APPLICANT: Gheysen, Dirk  
APPLICANT: Corixa Corporation  
APPLICANT: SmithKline Beecham Biologicals S. A.  
TITLE OF INVENTION: HER-2/neu Fusion Proteins  
FILE REFERENCE: 014058-009810PC  
CURRENT APPLICATION NUMBER: US/09/854,356  
CURRENT FILING DATE: 2001-05-09  
PRIOR APPLICATION NUMBER: US 09/493,480  
PRIOR FILING DATE: 2000-01-28  
PRIOR APPLICATION NUMBER: US 60/117,976  
PRIOR FILING DATE: 1999-01-29  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 1255  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: human HER-2/neu protein  
NAME/KEY: DOMAIN  
LOCATION: (1)..(653)  
OTHER INFORMATION: extracellular domain (ECD)  
NAME/KEY: DOMAIN  
LOCATION: (676)..(1255)  
OTHER INFORMATION: intracellular domain (ICD)  
NAME/KEY: DOMAIN  
LOCATION: (990)..(1255)  
OTHER INFORMATION: phosphorylation domain (PD)  
NAME/KEY: DOMAIN  
LOCATION: (990)..(1048)  
OTHER INFORMATION: fragment of the phosphorylation domain, preferred  
OTHER INFORMATION: portion (delta PD)  
US-09-854-356-1

Query Match 100.0%; Score 54; DB 10; Length 1255;  
Best Local Similarity 100.0%; Pred. No. 0.068;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EYLVPPQGF 10  
|||||

Db 1021 EYLVPPQGF 1030

Search completed: July 28, 2003, 17:14:58  
Job time : 51 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 28, 2003, 16:44:34 ; Search time 82 seconds  
(without alignments)  
19.357 Million cell updates/sec

Title: US-09-930-125-3  
Perfect score: 54  
Sequence: 1 EEVLVPQGF 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues  
Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54	100.0	10	AAE20480	Naturally processe
2	54	100.0	10	AAU77115	Human Her-2/neu im
3	54	100.0	59	AAU77115	Human Her-2/neu pr
4	54	100.0	59	AAU77115	Human Her-2/neu on
5	54	100.0	266	AAU77115	Human Her-2/neu pr
6	54	100.0	266	AAU77115	Human Her-2/neu on
7	54	100.0	293	AAU77115	Breast and ovarian
8	54	100.0	583	AAU77115	Human protein for
9	54	100.0	587	AAU77115	Human protein for

10	54	100.0	589	23	AAE20484	Human protein for
11	54	100.0	600	23	AAE20482	Human protein for
12	54	100.0	712	21	AAU77115	Human Her-2/neu fu
13	54	100.0	712	23	AAU77115	Her-2/neu extracel
14	54	100.0	919	21	AAU77115	Human Her-2/neu fu
15	54	100.0	919	23	AAU77115	Her-2/neu extracel
16	54	100.0	920	23	AAU77115	Mouse Her-2/neu ex
17	54	100.0	926	23	AAU77115	Mouse Her-2/neu ex
18	54	100.0	1200	21	AAU77115	Human Her-2/neu pr
19	54	100.0	1223	23	AAU77115	Human breast cance
20	54	100.0	1255	17	AAU77115	HER-2/neu protein.
21	54	100.0	1255	20	AAU77115	Human Her-2/neu on
22	54	100.0	1255	21	AAU77115	Human Her-2/neu pr
23	54	100.0	1255	21	AAU77115	Amino acid sequenc
24	54	100.0	1255	21	AAU77115	Human heregulin 2
25	54	100.0	1255	22	AAU77115	Human tyrosine kin
26	54	100.0	1255	22	AAU77115	Human Her-2/neu pr
27	54	100.0	1255	22	AAU77115	HER2/neu amino aci
28	54	100.0	1255	22	AAU77115	HER2 transgene pla
29	54	100.0	1255	23	AAU77115	Human Her-2 protei
30	54	100.0	1255	23	AAU77115	Human Her-2 antigen
31	54	100.0	1255	23	AAU77115	Human Her-2 protel
32	54	100.0	1255	23	AAU77115	Human Her-2/neu pr
33	54	100.0	1255	23	AAU77115	Human Her-2/neu po
34	54	100.0	1255	23	AAU77115	Human Her-2 (Erbb2)
35	54	100.0	1255	24	AAU77115	Breast cancer asso
36	54	100.0	1255	24	AAU77115	Human Her2/neu pro
37	54	100.0	1256	21	AAU77115	Rat HER-2/neu prot
38	54	100.0	1256	21	AAU77115	Mouse Her-2/neu pr
39	54	100.0	1256	22	AAU77115	Amino acid sequenc
40	54	100.0	1256	22	AAU77115	Rat Her-2/neu onco
41	54	100.0	1256	23	AAU77115	Sequence of c-erbB
42	54	100.0	1256	23	AAU77115	Inhibitor of TK of
43	54	100.0	1433	14	AAU77115	EGF-R derived pept
44	50	92.6	11	14	AAU77115	
45	50	92.6	13	16	AAU77115	

ALIGNMENTS

RESULT 1  
AAE20480  
ID AAE20480 standard; peptide; 10 AA.  
XX  
AC AAE20480;  
XX  
DT 01-JUL-2002 (first entry)  
XX  
DE Naturally processed HLA-B44-restricted epitope of human Her-2/neu.

Human; Her-2/Neu protein; immune response; gene therapy; breast cancer;  
human leukocyte antigen; HLA; vaccine; malignancy; cytostatic.

OS Homo sapiens.

PN WO200214503-A2.

XX 21-FEB-2002.

PD 14-AUG-2001; 2001WO-US41733.

XX 14-AUG-2000; 2000US-225152P.

PR 28-SEP-2000; 2000US-236428P.

PR 21-FEB-2001; 2001US-270520P.

(CORI-) CORIXA CORP.

Hand-zimmermann S, Cheever MA, Foy TM, Lodes MJ, Kalos MD;  
McNeill PD, Vedvick TS;

WPI; 2002-280758/32.

PT Novel isolated Her-2/Neu polypeptide composition useful for therapy,  
 PT prevention and diagnosis of cancer, preferably breast cancer  
 XX  
 PS Claim 2; Page 87; 129pp; English.  
 XX  
 CC The invention relates to an isolated Her-2/Neu polypeptide composition  
 CC effective for eliciting an immune response. The invention is useful for  
 CC eliciting an immune response in a patient, where the patient is human  
 CC leukocyte antigen (HLA)-B44 positive or is affected with breast cancer.  
 CC The composition is useful for the therapy and diagnosis of cancer,  
 CC preferably breast cancer, in pharmaceutical compositions, e.g., vaccine  
 CC and other compositions for the diagnosis, prevention and treatment of  
 CC human malignancies, for stimulating and/or expanding T cells specific for  
 CC Her-2/Neu polypeptide and for inhibiting the development of cancer in a  
 CC patient. The invention is useful for stimulating a T cell response in a  
 CC human patient, as probe or primer for nucleic acid hybridisation, to  
 CC selectively form duplex molecules with complementary stretches of the  
 CC entire Her-2/Neu gene or gene fragments of interest, to isolate a full  
 CC length gene from a suitable library, and to direct expression of a  
 CC polypeptide in appropriate host-cells. The composition is useful in  
 CC prophylactic or therapeutic applications and for the treatment of cancer,  
 CC preferably for the immunotherapy of breast cancer and other Her-2/Neu-  
 CC associated malignancies. The invention is useful in gene therapy. The  
 CC present sequence is naturally processed HLA-B44-restricted epitope of  
 CC human Her-2/Neu protein.  
 XX  
 SQ Sequence 10 AA;  
 Query Match 100.0%; Score 54; DB 23; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.0041;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EBYLVPQQGF 10  
 Db |||||||||  
 1 EBYLVPQQGF 10  
 RESULT 2  
 AAU77115  
 ID AAU77115 standard; Peptide; 10 AA.  
 AC  
 XX  
 XX AAU77115;  
 DT  
 XX 05-JUN-2002 (first entry)  
 DE Human Her-2/Neu immunogenic epitope.  
 XX  
 KW Human; Her-2/Neu; cytostatic; haematological malignancy; CML;  
 KW acute myelogenous leukaemia; AML; chronic myelogenous leukaemia; CLL;  
 KW chronic lymphocytic leukaemia; myeloma; non-Hodgkin's lymphoma; MDS;  
 KW Hodgkin's lymphoma; T cell therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200213847-A2.  
 XX  
 XX 21-FEB-2002.  
 PD  
 XX 13-AUG-2001; 2001WO-US25408.  
 PF  
 XX 14-AUG-2000; 2000US-0638280.  
 PR  
 XX 28-SEP-2000; 2000US-0675904.  
 XX  
 PA (CORI-) CORIXA CORP.  
 XX  
 PI Gaiger A, Cheever MA, Hand-zimmermann S;  
 XX  
 DR WPI; 2002-280741/32.  
 XX  
 XX Inhibiting haematological malignancy development by administering  
 PT polypeptide comprising immunogenic portion of Her-2/Neu, polynucleotide  
 PT encoding the polypeptide, or antigen presenting cells expressing the  
 PT polypeptide

XX  
 PS Claim 2; Page 49; 74pp; English.  
 XX  
 CC The invention relates to a method for inhibiting development of  
 CC haematological malignancy in a patient by administering a polypeptide  
 CC comprising an immunogenic portion of Her-2/Neu or a polynucleotide  
 CC encoding the polypeptide. Antigen presenting cells that express the  
 CC protein can also be administered. The sequences are used for inhibiting  
 CC development of haematological malignancy such as acute myelogenous  
 CC leukaemia (AML), chronic myelogenous leukaemia (CML), chronic lymphocytic  
 CC leukaemia (CLL), MDS, myelomas, Hodgkin's lymphoma and non-Hodgkin's  
 CC lymphoma. This sequence represents a human Her-2/Neu immunogenic epitope.  
 XX  
 SQ Sequence 10 AA;  
 Query Match 100.0%; Score 54; DB 23; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.0041;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EBYLVPQQGF 10  
 Db |||||||||  
 1 EBYLVPQQGF 10  
 RESULT 3  
 AAB21202  
 ID AAB21202 standard; protein; 59 AA.  
 XX  
 XX AAB21202;  
 AC  
 XX  
 XX 12-JAN-2001 (first entry)  
 DT  
 XX Human HER-2/Neu protein phosphorylation domain partial sequence.  
 DE  
 XX Human; HER-2/Neu; oncogene; tyrosine kinase; cytostatic; vaccine;  
 KW breast cancer; prostate cancer; ovarian cancer; lung cancer;  
 KW colon cancer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200044899-A1.  
 XX  
 XX 03-AUG-2000.  
 PD  
 XX 28-JAN-2000; 2000WO-US02164.  
 PF  
 XX 29-JAN-1999; 99US-0117976.  
 XX  
 PR (CORI-) CORIXA CORP.  
 XX  
 PA (SMIK ) SMITHKLINE BEECHAM.  
 XX  
 PI Cheever MA, Gheysen D;  
 XX  
 XX WPI; 2000-505976/45.  
 DR  
 XX HER-2/Neu extracellular domain/phosphorylation domain fusion proteins  
 PT useful for vaccinating against breast, ovarian, colon, lung and  
 PT prostate cancers -  
 XX  
 PS Claim 27; Fig 11; 128pp; English.  
 XX  
 CC The present sequence is a preferred portion of the phosphorylation domain  
 CC of the HER-2/Neu protein. HER-2/Neu is a member of the tyrosine kinase  
 CC family of receptor-like glycoproteins and shows homology to the epidermal  
 CC growth factor receptor (EGFR). It probably plays a part in cell growth  
 CC and/or differentiation. The HER-2/Neu gene is an oncogene. An HER-2/Neu  
 CC fusion protein comprising a HER-2/Neu extracellular domain fused to a  
 CC HER-2/Neu phosphorylation domain may be used to treat or prevent cancer  
 CC by eliciting or enhancing an immune response to the HER-2/Neu protein. It  
 CC may be used to treat malignancies such as breast, ovarian, colon, lung  
 CC and prostate cancers, and may be used as an antigen to vaccinate against  
 CC these neoplasias.

Tue Jul 29 09:32:16 2003

CC fusion protein can be used to remove tumour cells from a sample in  
 CC order to inhibit the development of cancer in a patient.  
 XX  
 SQ Sequence 59 AA;  
 Query Match 100.0%; Score 54; DB 21; Length 59;  
 Best Local Similarity 100.0%; Pred. No. 0.023;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EYLVPPQGGF 10  
 |||||  
 DB 32 EYLVPPQGGF 41

RESULT 4  
 RAM51147  
 ID AAM51147 standard; Protein; 59 AA.  
 XX  
 AC AAM51147;  
 XX  
 DT 17-JUN-2002 (first entry)  
 XX  
 DE Human Her-2/neu oncoprotein phosphorylation domain fragment.  
 XX  
 KW Her-2/neu; oncogene; cancer; tumour; vaccine; human; p185;  
 XX  
 KW tyrosine kinase; receptor; c-erbB2; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200212341-A2.  
 XX  
 PD 14-FEB-2002.  
 XX  
 PF 03-AUG-2001; 2001WO-US24283.  
 XX  
 PR 03-AUG-2000; 2000US-0632507.  
 XX  
 PA (CORI-) CORIXA CORP.  
 XX  
 PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.  
 XX  
 PI Cheever MA, Gheysen D;  
 XX  
 DR WPI; 2002-241743/29.  
 XX  
 PT Her-2/neu fusion protein for treating or preventing cancer by eliciting  
 PT or enhancing an immune response to the protein, has Her-2/neu  
 PT extracellular domain fused to Her-2/neu intracellular or  
 PT phosphorylation domain  
 XX  
 PS Disclosure; Fig 11; 141pp; English.

CC The present sequence is that of a fragment (DeltaPp) of the  
 CC phosphorylation domain of human Her-2/neu (p185 glycoprotein,  
 CC c-erbB2), an oncogenic self-protein and target for anti-cancer  
 CC vaccines. The Her-2/neu gene is amplified and p185 is  
 CC overexpressed in breast, ovarian, colon, lung and prostate cancer.  
 CC Her-2/neu (see AAM51143) is a member of the tyrosine kinase family  
 CC of receptor-like glycoproteins. It comprises an extracellular  
 CC domain with homology to the epidermal growth factor receptor  
 CC (EGFR), a highly hydrophobic transmembrane domain and a C-terminal  
 CC intracellular domain that also shows homology to EGFR. Its  
 CC overexpression correlates with a poor prognosis in breast and  
 CC ovarian cancers. The invention provides Her-2/neu fusion  
 CC proteins, nucleic acids encoding them, viral vectors, and vaccines  
 CC comprising the fusion proteins or nucleic acid molecules. In  
 CC preferred fusion proteins, the extracellular domain of a Her-2/neu  
 CC protein is fused to a Her-2/neu intracellular domain or  
 CC phosphorylation domain (or the DeltaPp fragment). An immune  
 CC response to Her-2/neu protein is elicited or enhanced by  
 CC administering the fusion protein in the form of a vaccine, or by  
 CC administering cells of an animal *ex vivo* with a nucleic acid  
 CC encoding the fusion protein, and delivering the transfected cells  
 CC to the animal. The fusion proteins, nucleic acids, and isolated  
 CC specific T-cells are useful for inhibiting the development of a  
 CC cancer, especially breast, ovarian, colon, lung or prostate cancer  
 CC in a patient. T cells that specifically react with a Her-2/neu

CC fusion protein can be used to remove tumour cells from a sample in  
 CC order to inhibit the development of cancer in a patient.  
 XX  
 SQ Sequence 59 AA;  
 Query Match 100.0%; Score 54; DB 23; Length 59;  
 Best Local Similarity 100.0%; Pred. No. 0.023;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EYLVPPQGGF 10  
 |||||  
 DB 32 EYLVPPQGGF 41

RESULT 5  
 AAB21201  
 ID AAB21201 standard; protein; 266 AA.  
 XX  
 AC AAB21201;  
 XX  
 DT 12-JAN-2001 (first entry)  
 XX  
 DE Human HER-2/neu protein phosphorylation domain.  
 XX  
 KW Human; HER-2/neu; oncogene; tyrosine kinase; cytostatic; vaccine;  
 XX  
 KW breast cancer; prostate cancer; ovarian cancer; lung cancer;  
 XX  
 KW colon cancer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200044899-A1.  
 XX  
 PD 03-AUG-2000.  
 XX  
 PF 28-JAN-2000; 2000WO-US02164.  
 XX  
 PR 29-JAN-1999; 99US-0117976.  
 XX  
 PA (CORI-) CORIXA CORP.  
 XX  
 PA (SMIK) SMITHKLINE BEECHAM.  
 XX  
 PI Cheever MA, Gheysen D;  
 XX  
 DR WPI; 2000-505976/45.  
 XX  
 PT HER-2/neu extracellular domain/phosphorylation domain fusion proteins  
 PT useful for vaccinating against breast, ovarian, colon, lung and  
 PT prostate cancers  
 XX  
 PS Claim 2; Fig 10; 128pp; English.

CC The present sequence is the phosphorylation domain of the HER-2/neu  
 CC protein. HER-2/neu is a member of the tyrosine kinase family of  
 CC receptor-like glycoproteins and shows homology to the epidermal growth  
 CC factor receptor (EGFR). It probably plays a part in cell growth and/or  
 CC differentiation. The HER-2/neu gene is an oncogene. An HER-2/neu fusion  
 CC protein comprising a HER-2/neu extracellular domain fused to a HER-2/neu  
 CC phosphorylation domain may be used to treat or prevent cancer by  
 CC eliciting or enhancing an immune response to the HER-2/neu protein. It  
 CC may be used to treat malignancies such as breast, ovarian, colon, lung  
 CC and prostate cancers, and may be used as an antigen to vaccinate against  
 CC these neoplasias.

CC Sequence 266 AA;  
 Query Match 100.0%; Score 54; DB 21; Length 266;  
 Best Local Similarity 100.0%; Pred. No. 0.1;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EYLVPPQGGF 10  
 |||||  
 DB 32 EYLVPPQGGF 41



RESULT 6  
 AAM51146  
 ID AAM51146 standard; Protein; 266 AA.  
 AC AAM51146;  
 DT 17-JUN-2002 (first entry)  
 DE Human Her-2/neu oncoprotein phosphorylation domain.  
 DE Her-2/neu; oncogene; cancer; tumour; vaccine; human; p185;  
 KW tyrosine kinase; receptor; c-erbB2; gene therapy.  
 XX Homo sapiens.  
 XX WO200212341-A2.  
 PD 14-FEB-2002.  
 XX 03-AUG-2001; 2001WO-US24283.  
 XX 03-AUG-2000; 2000US-0632507.  
 PR (CORI-) CORIXA CORP.  
 PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
 XX Cheever MA, Gheysen D;  
 XX WPI; 2002-241743/29.  
 DR Her-2/neu fusion protein for treating or preventing cancer by eliciting  
 XX or enhancing an immune response to the protein, has Her-2/neu  
 PT extracellular domain fused to Her-2/neu intracellular or  
 PT phosphorylation domain  
 XX Claim 2; Fig 10; 141pp; English.  
 PS The present sequence is that of the phosphorylation domain of  
 CC human Her-2/neu (p185 glycoprotein or c-erbB2), an oncogenic  
 CC self-protein and target for anti-cancer vaccines. The Her-2/neu  
 CC gene is amplified and p185 is overexpressed in a variety of cancers,  
 CC including breast, ovarian, colon, lung and prostate cancer.  
 CC Her-2/neu (see AAM51143) is a member of the tyrosine kinase family  
 CC of receptor-like glycoproteins. It comprises an extracellular  
 CC domain with homology to the epidermal growth factor receptor  
 CC (EGFR), a highly hydrophobic transmembrane domain and a C-terminal  
 CC intracellular domain that also shows homology to EGFR. Its  
 CC overexpression correlates with a poor prognosis in breast and  
 CC ovarian cancers. The invention provides Her-2/neu fusion  
 CC proteins, nucleic acids encoding them, viral vectors, and vaccines  
 CC comprising the fusion proteins or nucleic acid molecules. In  
 CC preferred fusion proteins, the extracellular domain of a Her-2/neu  
 CC protein is fused to a Her-2/neu intracellular domain or  
 CC phosphorylation domain (or its DeltaCD fragment). An immune  
 CC response to Her-2/neu protein is elicited or enhanced by  
 CC administering the fusion protein in the form of a vaccine, or by  
 CC transfecting cells of an animal *ex vivo* with a nucleic acid  
 CC encoding the fusion protein, and delivering the transfected cells  
 CC to the animal. The fusion proteins, nucleic acids, and isolated  
 CC specific T-cells are useful for inhibiting the development of a  
 CC cancer, especially breast, ovarian, colon, lung or prostate cancer  
 CC in a patient. T cells that specifically react with a Her-2/neu  
 CC fusion protein can be used to remove tumour cells from a sample in  
 CC order to inhibit the development of cancer in a patient.  
 XX Sequence 266 AA;  
 SQ Query Match 100.0%; Score 54; DB 23; Length 266;  
 Best Local Similarity 100.0%; Pred. No. 0.1;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EYLVPPQGF 10

Db 32 EYLVPPQGF 41  
 RESULT 7  
 AAB58875  
 ID AAB58875 standard; Protein; 293 AA.  
 XX AAB58875;  
 AC AAB58875;  
 DT 27-MAR-2001 (first entry)  
 DE Breast and ovarian cancer associated antigen protein sequence SEQ ID 583.  
 XX Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;  
 KW neoplastic; neuroprotective; antiviral; antiallergic; hepatotropic;  
 KW antidiabetic; antiinflammatory; antitumor; vulnary; anticonvulsant;  
 KW antibacterial; antifungal; antiparasitic; cardiac; immune disorder;  
 KW Addison's disease; allergy; autoimmune haemolytic anaemia;  
 KW autoimmune thyroiditis; diabetes mellitus; Crohn's disease;  
 KW multiple sclerosis; rheumatoid arthritis; ulcerative colitis;  
 KW cardiovascular disorder; wound healing; neurological disease.  
 XX Homo sapiens.  
 OS WO200055173-A1.  
 PN 21-SEP-2000.  
 PD 08-MAR-2000; 2000WO-US05881.  
 XX 12-MAR-1999; 99US-0124270.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA Rosen CA, Ruben SM;  
 PI WPI; 2000-611515/58.  
 DR N-PSDB; AAF21778.  
 XX New human breast and ovarian cancer associated gene sequences and the  
 PT polypeptides encoded by these genes, useful in the prevention,  
 PT treatment and diagnosis of cancer, immune disorders, cardiovascular  
 PT disorders and neurological diseases -  
 XX Claim 11; Page 1019-1020; 1299pp; English.  
 PS Sequences AAF21614 - AAF22031 represent DNA sequences encoding human  
 CC proteins AAB58711 - AAB59128. The DNA and protein sequences are  
 CC associated with breast and ovarian cancer. Included in the invention are  
 CC sequences AAF22032 - AAF22040 and AAB59129 which are used in the  
 CC isolation and characterisation of the DNA and protein sequences of the  
 CC invention. The breast and ovarian cancer associated DNA, protein, agonist  
 CC or antagonist sequences exhibit cytostatic; immunosuppressive;  
 CC neoplastic; neuroprotective; antiviral; antiallergic; hepatotropic;  
 CC antidiabetic; antiinflammatory; antitumor; vulnary; anticonvulsant;  
 CC antibacterial; antifungal; antiparasitic and cardiac activity. The  
 CC polynucleotide and protein sequences are used in the diagnosis of cancer,  
 CC particularly breast and ovarian cancer. The nucleic acid sequences,  
 CC proteins, agonists and antagonists may also be used in the diagnosis,  
 CC prevention and treatment of immune disorders e.g. Addison's disease,  
 CC allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,  
 CC diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid  
 CC arthritis and ulcerative colitis; cardiovascular disorders such as  
 CC myocardial ischaemia; wound healing; neurological diseases such as  
 CC cerebral anoxia and epilepsy; and infectious diseases.  
 XX Sequence 293 AA;  
 SQ Query Match 100.0%; Score 54; DB 21; Length 293;  
 Best Local Similarity 100.0%; Pred. No. 0.11;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EBYLVPQOGF 10  
Db 105 EBYLVPQOGF 114

RESULT 8  
AAE20483  
ID AAE20483 standard; Protein; 583 AA.  
AC AAE20483;  
XX  
DT 01-JUL-2002 (first entry)  
XX  
XX Human protein for the clone HICD\_native\_coding\_region.

DE Human; Her-2/Neu protein; immune response; gene therapy; breast cancer;  
KW human leukocyte antigen; HLA; vaccine; malignancy; cytostatic.  
XX  
XX Homo sapiens.  
OS  
XX  
XX Key Location/Qualifiers  
FH Misc-difference 581..583  
FT /note= "Encoded by GTGTAATGACGC"  
XX  
XX WO200214503-A2.  
XX  
XX 21-FEB-2002.

XX 14-AUG-2001; 2001WO-US41733.  
XX  
XX 14-AUG-2000; 2000US-225152P.  
PR 28-SEP-2000; 2000US-236428P.  
PR 21-FEB-2001; 2001US-270520P.  
XX  
XX (CORI-) CORIXA CORP.  
XX  
XX Hand-zimmermann S, Cheever MA, Foy TM, Lodes MJ, Kalos MD;  
PI McNeill PD, Vedvick TS;  
XX  
XX WPI: 2002-280758/32.  
DR N-PSDB; AAD32746.  
XX  
XX Novel isolated Her-2/Neu polypeptide composition useful for therapy,  
PT prevention and diagnosis of cancer, preferably breast cancer  
XX  
XX Example 5; Page 121-122; 129pp; English.

XX The invention relates to an isolated Her-2/Neu polypeptide composition  
CC effective for eliciting an immune response. The invention is useful for  
CC eliciting an immune response in a patient, where the patient is human  
CC leukocyte antigen (HLA)-B44 positive or is affected with breast cancer.  
CC The composition is useful for the therapy and diagnosis of cancer.  
CC preferably breast cancer, in pharmaceutical compositions, e.g., vaccine  
CC and other compositions for the diagnosis, prevention and treatment of  
CC human malignancies, for stimulating and/or expanding T cells specific for  
CC Her-2/Neu polypeptide and for inhibiting the development of cancer in a  
CC patient. The invention is useful for stimulating a T cell response in a  
CC human patient, as probe or primer for nucleic acid hybridisation, to  
CC selectively form duplex molecules with complementary stretches of the  
CC entire Her-2/Neu gene or gene fragments of interest, to isolate a full  
CC length gene from a suitable library, and to direct expression of a  
CC polypeptide in appropriate host cells. The composition is useful in  
CC prophylactic or therapeutic applications and for the treatment of cancer,  
CC preferably for the immunotherapy of breast cancer and other Her-2/Neu-  
CC associated malignancies. The invention is useful in gene therapy. The  
CC present sequence is human protein for the clone HICD\_native\_coding\_  
XX region.

SQ Sequence 583 AA;  
Query Match 100.0%; Score 54; DB 23; Length 583;  
Best Local Similarity 100.0%; Pred. No. 0.22;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EBYLVPQOGF 10  
Db 347 EBYLVPQOGF 356

RESULT 9  
AAE20481  
ID AAE20481 standard; Protein; 587 AA.  
XX  
AC AAE20481;  
XX  
DT 01-JUL-2002 (first entry)  
XX  
XX Human protein for the clone HICD\_CT\_His\_coding\_region.

DE Human; Her-2/Neu protein; immune response; gene therapy; breast cancer;  
KW human leukocyte antigen; HLA; vaccine; malignancy; cytostatic.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200214503-A2.  
XX  
XX 21-FEB-2002.

XX 14-AUG-2001; 2001WO-US41733.  
XX  
XX 14-AUG-2000; 2000US-225152P.  
PR 28-SEP-2000; 2000US-236428P.  
PR 21-FEB-2001; 2001US-270520P.  
XX  
XX (CORI-) CORIXA CORP.  
XX  
XX Hand-zimmermann S, Cheever MA, Foy TM, Lodes MJ, Kalos MD;  
PI McNeill PD, Vedvick TS;  
XX  
XX WPI: 2002-280758/32.  
DR N-PSDB; AAD32744.  
XX  
XX Novel isolated Her-2/Neu polypeptide composition useful for therapy,  
PT prevention and diagnosis of cancer, preferably breast cancer  
XX  
XX Example 5; Page 120-121; 129pp; English.

XX The invention relates to an isolated Her-2/Neu polypeptide composition  
CC effective for eliciting an immune response. The invention is useful for  
CC eliciting an immune response in a patient, where the patient is human  
CC leukocyte antigen (HLA)-B44 positive or is affected with breast cancer.  
CC The composition is useful for the therapy and diagnosis of cancer,  
CC preferably breast cancer, in pharmaceutical compositions, e.g., vaccine  
CC and other compositions for the diagnosis, prevention and treatment of  
CC human malignancies, for stimulating and/or expanding T cells specific for  
CC Her-2/Neu polypeptide and for inhibiting the development of cancer in a  
CC patient. The invention is useful for stimulating a T cell response in a  
CC human patient, as probe or primer for nucleic acid hybridisation, to  
CC selectively form duplex molecules with complementary stretches of the  
CC entire Her-2/Neu gene or gene fragments of interest, to isolate a full  
CC length gene from a suitable library, and to direct expression of a  
CC polypeptide in appropriate host cells. The composition is useful in  
CC prophylactic or therapeutic applications and for the treatment of cancer,  
CC preferably for the immunotherapy of breast cancer and other Her-2/Neu-  
CC associated malignancies. The invention is useful in gene therapy. The  
CC present sequence is human protein for the clone HICD\_CT\_His\_coding\_  
XX region.

SQ Sequence 587 AA;  
Query Match 100.0%; Score 54; DB 23; Length 587;  
Best Local Similarity 100.0%; Pred. No. 0.22;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EBYLVPQOGF 10  
Db 105 EBYLVPQOGF 114

Db 347 EYLVPOQGF 356

RESULT 10.  
AAE20484  
ID AAE20484 standard; Protein; 589 AA.  
XX AC AAE20484;  
XX DT 01-JUL-2002 (first entry)  
XX DE Human protein for clone HICD\_in\_ppdm\_coding\_sequence.  
XX KW Human; Her-2/Neu protein; immune response; gene therapy; breast cancer;  
XX KW human leukocyte antigen; HLA; vaccine; malignancy; cytostatic.  
XX OS Homo sapiens.  
XX PN WO200214503-A2.  
XX PD 21-FEB-2002.  
XX PF 14-AUG-2001; 2001WO-US41733.  
XX PR 14-AUG-2000; 2000US-225152P.  
XX PR 28-SEP-2000; 2000US-236428P.  
XX PR 21-FEB-2001; 2001US-270520P.  
XX PA (CORI-) CORIXA CORP.  
XX PI Hand-zimmermann S, Cheever MA, Foy TM, Lodes MJ, Kalos MD;  
XX PI McNeill PD, Vedvick TS;  
XX DR WPI; 2002-280758/32.  
XX DR N-PSDB; AAD32747.  
XX PT Novel isolated Her-2/Neu polypeptide composition useful for therapy,  
XX PT prevention and diagnosis of cancer, preferably breast cancer -  
XX PS Example 5; Page 122-123; 129pp; English.  
XX CC The invention relates to an isolated Her-2/Neu polypeptide composition  
XX CC effective for eliciting an immune response. The invention is useful for  
XX CC eliciting an immune response in a patient, where the patient is human  
XX CC leukocyte antigen (HLA)-B44 positive or is affected with breast cancer.  
XX CC The composition is useful for the therapy and diagnosis of cancer.  
XX CC preferably breast cancer, in pharmaceutical compositions, e.g., vaccine  
XX CC and other compositions for the diagnosis, prevention and treatment of  
XX CC human malignancies, for stimulating and/or expanding T cells specific for  
XX CC Her-2/Neu polypeptide and for inhibiting the development of cancer in a  
XX CC patient. The invention is useful for stimulating a T cell response in a  
XX CC human patient, as probe or primer for nucleic acid hybridisation, to  
XX CC selectively form duplex molecules with complementary stretches of the  
XX CC entire Her-2/Neu gene or gene fragments of interest, to isolate a full  
XX CC length gene from a suitable library, and to direct expression of a  
XX CC polypeptide in appropriate host cells. The composition is useful in  
XX CC prophylactic or therapeutic applications and for the treatment of cancer,  
XX CC preferably for the immunotherapy of breast cancer and other Her-2/Neu-  
XX CC associated malignancies. The invention is useful in gene therapy. The  
XX CC present sequence is human protein for the clone HICD\_in\_ppdm\_coding\_  
XX SQ Sequence 589 AA;  
Query Match 100.0%; Score 54; DB 23; Length 589;  
Best Local Similarity 100.0%; Pred. No. 0.22;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EYLVPOQGF 10  
Db 355 EYLVPOQGF 364

RESULT 11  
AAE20482  
ID AAE20482 standard; Protein; 600 AA.  
XX AC AAE20482;  
XX DT 01-JUL-2002 (first entry)  
XX DE Human protein for the clone HICD\_plus\_8\_HIS.  
XX KW Human; Her-2/Neu protein; immune response; gene therapy; breast cancer;  
XX KW human leukocyte antigen; HLA; vaccine; malignancy; cytostatic.  
XX OS Homo sapiens.  
XX PN WO200214503-A2.  
XX PD 21-FEB-2002.  
XX PF 14-AUG-2001; 2001WO-US41733.  
XX PR 14-AUG-2000; 2000US-225152P.  
XX PR 28-SEP-2000; 2000US-236428P.  
XX PR 21-FEB-2001; 2001US-270520P.  
XX PA (CORI-) CORIXA CORP.  
XX PI Hand-zimmermann S, Cheever MA, Foy TM, Lodes MJ, Kalos MD;  
XX PI McNeill PD, Vedvick TS;  
XX DR WPI; 2002-280758/32.  
XX DR N-PSDB; AAD32745.  
XX PT Novel isolated Her-2/Neu polypeptide composition useful for therapy,  
XX PT prevention and diagnosis of cancer, preferably breast cancer -  
XX PS Example 5; Page 124-125; 129pp; English.  
XX CC The invention relates to an isolated Her-2/Neu polypeptide composition  
XX CC effective for eliciting an immune response. The invention is useful for  
XX CC eliciting an immune response in a patient, where the patient is human  
XX CC leukocyte antigen (HLA)-B44 positive or is affected with breast cancer.  
XX CC The composition is useful for the therapy and diagnosis of cancer,  
XX CC preferably breast cancer, in pharmaceutical compositions, e.g., vaccine  
XX CC and other compositions for the diagnosis, prevention and treatment of  
XX CC human malignancies, for stimulating and/or expanding T cells specific for  
XX CC Her-2/Neu polypeptide and for inhibiting the development of cancer in a  
XX CC patient. The invention is useful for stimulating a T cell response in a  
XX CC human patient, as probe or primer for nucleic acid hybridisation, to  
XX CC selectively form duplex molecules with complementary stretches of the  
XX CC entire Her-2/Neu gene or gene fragments of interest, to isolate a full  
XX CC length gene from a suitable library, and to direct expression of a  
XX CC polypeptide in appropriate host cells. The composition is useful in  
XX CC prophylactic or therapeutic applications and for the treatment of cancer,  
XX CC preferably for the immunotherapy of breast cancer and other Her-2/Neu-  
XX CC associated malignancies. The invention is useful in gene therapy. The  
XX CC present sequence is human protein for the clone HICD\_plus\_8\_HIS.  
XX SQ Sequence 600 AA;  
Query Match 100.0%; Score 54; DB 23; Length 600;  
Best Local Similarity 100.0%; Pred. No. 0.22;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EYLVPOQGF 10  
Db 366 EYLVPOQGF 375

## RESULT 12

AAB21204  
ID AAB21204 standard; protein; 712 AA.

XX  
AC AAB21204;

XX  
DT 12-JAN-2001 (first entry)

XX  
DE Human HER-2/neu fusion protein.

XX  
KW Human; HER-2/neu; oncogene; tyrosine kinase; cytostatic; vaccine;  
breast cancer; prostate cancer; ovarian cancer; lung cancer;  
colon cancer; fusion protein.

XX  
OS Homo sapiens.

XX  
OS Synthetic.

XX  
PN WO200044899-A1.

XX  
PD 03-AUG-2000.

XX  
PF 28-JAN-2000; 2000WO-US02164.

XX  
PR 29-JAN-1999; 99US-0117976.

XX  
PA (CORI-) CORIXA CORP.

XX  
PA (SMIK ) SMITHKLINE BEECHAM.

XX  
PI Cheever MA, Gheysen D;

XX  
PI WPI; 2000-505976/45.

XX  
PT HER-2/neu extracellular domain/phosphorylation domain fusion proteins  
useful for vaccinating against breast, ovarian, colon, lung and  
prostate cancers -

XX  
PS Claim 27; Fig 13; 128pp; English.

XX  
CC The present sequence is a fusion protein comprising the extracellular  
domain and a preferred portion of the phosphorylation domain of the human  
HER-2/neu protein. HER-2/neu is a member of the tyrosine kinase family of  
receptor-like glycoproteins and shows homology to the epidermal growth  
factor receptor (EGFR). It probably plays a part in cell growth and/or  
differentiation. The HER-2/neu gene is an oncogene. HER-2/neu fusion  
proteins may be used to treat or prevent cancer by eliciting or enhancing  
an immune response to the HER-2/neu protein. They may be used to treat  
malignancies such as breast, ovarian, colon, lung and prostate cancers,  
and may be used as an antigen to vaccinate against these neoplasias.

XX  
SQ Sequence 712 AA;

Query Match 100.0%; Score 54; DB 21; Length 712;  
Best Local Similarity 100.0%; Pred. No. 0.26;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EEYLVPPQGF 10  
|||||  
Db 685 EEYLVPPQGF 694

## RESULT 13

AAM51149  
ID AAM51149 standard; Protein; 712 AA.

XX  
AC AAM51149;

XX  
DT 17-JUN-2002 (first entry)

XX  
DE Her-2/neu extracellular domain-delta-phosphorylation domain fusion.

XX  
KW Her-2/neu; oncogene; cancer; tumour; vaccine; human; p185;

XX  
KW tyrosine kinase; receptor; c-erbB2; gene therapy.

OS Homo sapiens.

XX  
FH Key Location/Qualifiers  
FT Domain 1..653

FT /note= "extracellular domain"  
FT Domain 654..712  
FT /note= "phosphorylation domain fragment"

XX  
PN WO200212341-A2.

XX  
PD 14-FEB-2002.

XX  
PF 03-AUG-2001; 2001WO-US24283.

XX  
PR 03-AUG-2000; 2000US-0632507.

XX  
PA (CORI-) CORIXA CORP.  
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.

XX  
PI Cheever MA, Gheysen D;

XX  
PI WPI; 2002-241743/29.

XX  
PT Her-2/neu fusion protein for treating or preventing cancer by eliciting  
or enhancing an immune response to the protein, has Her-2/neu  
extracellular domain fused to Her-2/neu intracellular or  
phosphorylation domain -

XX  
PS Claim 37; Fig 13; 141pp; English.

XX  
CC The present sequence is that of a fusion protein between the  
extracellular domain and a fragment (DeltapD) of the phosphorylation  
domain of human Her-2/neu (see AAM51143), an oncogenic self-protein  
and target for anti-cancer vaccines. The fusion protein can be  
obtained by recombinant DNA methods. Her-2/neu overexpression  
correlates with a poor prognosis in breast and ovarian cancers.  
The invention provides Her-2/neu fusion proteins, nucleic acids  
encoding them, viral vectors, and vaccines comprising the fusion  
proteins or nucleic acid molecules. In preferred fusion proteins,  
the extracellular domain of Her-2/neu is fused to a Her-2/neu  
intracellular domain or phosphorylation domain (or its DeltapD  
fragment). An immune response to Her-2/neu protein is elicited or  
enhanced by administering the fusion protein in the form of a vaccine,  
or by transfecting cells of an animal ex vivo with a nucleic acid  
encoding the fusion protein, and delivering the transfected cells  
to the animal. The fusion proteins, nucleic acids, and isolated  
specific T-cells are useful for inhibiting the development of a  
cancer, especially breast, ovarian, colon, lung or prostate cancer  
in a patient. T cells that specifically react with a Her-2/neu  
fusion protein can be used to remove tumour cells from a sample in  
order to inhibit the development of cancer in a patient.

XX  
SQ Sequence 712 AA;

Query Match 100.0%; Score 54; DB 23; Length 712;  
Best Local Similarity 100.0%; Pred. No. 0.26;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EEYLVPPQGF 10  
|||||  
Db 685 EEYLVPPQGF 694

## RESULT 14

AAB21203  
ID AAB21203 standard; protein; 919 AA.

XX  
AC AAB21203;

XX  
DT 12-JAN-2001 (first entry)

XX  
DE Human HER-2/neu fusion protein.

KW Human; HER-2/neu; oncogene; tyrosine kinase; cytostatic; vaccine;  
 KW breast cancer; prostate cancer; ovarian cancer; lung cancer;  
 KW colon cancer; fusion protein.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200044899-A1.  
 XX  
 PD 03-AUG-2000.  
 XX  
 PF 28-JAN-2000; 2000WO-US02164.  
 XX  
 PR 29-JAN-1999; 99US-0117976.  
 XX  
 PA (CORI-) CORIXA CORP.  
 PA (SMIK ) SMITHKLINE BEECHAM.  
 XX  
 PI Cheever MA, Gheysen D;  
 XX  
 PS WPI; 2000-505976/45.  
 DR  
 XX  
 XX HER-2/neu extracellular domain/phosphorylation domain fusion proteins  
 PT useful for vaccinating against breast, ovarian, colon, lung and  
 PT prostate cancers -  
 XX  
 PS Claim 2; Fig 12; 128pp; English.  
 XX  
 CC The present sequence is a fusion protein comprising the extracellular  
 CC domain and the phosphorylation domain of the human HER-2/neu protein.  
 CC HER-2/neu is a member of the tyrosine kinase family of receptor-like  
 CC glycoproteins and shows homology to the epidermal growth factor receptor  
 CC (EGFR). It probably plays a part in cell growth and/or differentiation.  
 CC The HER-2/neu gene is an oncogene. HER-2/neu fusion proteins may be used  
 CC to treat or prevent cancer by eliciting or enhancing an immune response  
 CC to the HER-2/neu protein. They may be used to treat malignancies such as  
 CC breast, ovarian, colon, lung and prostate cancers, and may be used as an  
 CC antigen to vaccinate against these neoplasias.  
 XX  
 XX Sequence 919 AA;  
 SQ  
 Query Match 100.0%; Score 54; DB 21; Length 919;  
 Best Local Similarity 100.0%; Pred. No. 0.34;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EYLVPPQGGF 10  
 Db |||||  
 685 EYLVPPQGGF 694  
 RESULT 15  
 AAM51148  
 ID AAM51148 standard; Protein; 919 AA.  
 XX  
 AC AAM51148;  
 XX  
 DT 17-JUN-2002 (first entry)  
 DE  
 XX Her-2/neu extracellular domain-phosphorylation domain fusion.  
 KW Her-2/neu; oncogene; cancer; tumour; vaccine; human; p185;  
 KW tyrosine kinase; receptor; c-erbB2; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PH Key Location/Qualifiers  
 FT Domain 1..653  
 FT /note= "extracellular domain"  
 FT Domain 654..919  
 FT /note= "phosphorylation domain"  
 XX  
 PN WO200212341-A2.  
 XX

PD 14-FEB-2002.  
 XX  
 PF 03-AUG-2001; 2001WO-US24283.  
 XX  
 PR 03-AUG-2000; 2000US-0632507.  
 XX  
 PA (CORI-) CORIXA CORP.  
 PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
 XX  
 PI Cheever MA, Gheysen D;  
 XX  
 PS WPI; 2002-241743/29.  
 DR  
 XX  
 XX Her-2/neu fusion protein for treating or preventing cancer by eliciting  
 PT or enhancing an immune response to the protein, has Her-2/neu  
 PT extracellular domain fused to Her-2/neu intracellular or  
 PT phosphorylation domain  
 XX  
 PS Claim 2; Fig 12; 141pp; English.  
 XX  
 CC The present sequence is that of a fusion protein between the  
 CC extracellular domain and phosphorylation domain of human Her-2/neu  
 CC (see AAM51143), an oncogenic self-protein and target for anti-cancer  
 CC vaccines. The fusion protein can be obtained by recombinant DNA  
 CC methods. Her-2/neu overexpression correlates with a poor prognosis  
 CC in breast and ovarian cancers. The invention provides Her-2/neu  
 CC fusion proteins, nucleic acids encoding them, viral vectors, and  
 CC vaccines comprising the fusion proteins or nucleic acid molecules.  
 CC In preferred fusion proteins, the extracellular domain of a  
 CC Her-2/neu protein is fused to a Her-2/neu intracellular domain or  
 CC phosphorylation domain (or its DeltapD fragment). An immune  
 CC response to Her-2/neu protein is elicited or enhanced by  
 CC administering the fusion protein in the form of a vaccine, or by  
 CC transfecting cells of an animal ex vivo with a nucleic acid  
 CC encoding the fusion protein, and delivering the transfected cells  
 CC to the animal. The fusion proteins, nucleic acids, and isolated  
 CC specific T-cells are useful for inhibiting the development of a  
 CC cancer, especially breast, ovarian, colon, lung or prostate cancer  
 CC in a patient. T cells that specifically react with a Her-2/neu  
 CC fusion protein can be used to remove tumour cells from a sample in  
 CC order to inhibit the development of cancer in a patient.  
 XX  
 SQ Sequence 919 AA;  
 Query Match 100.0%; Score 54; DB 23; Length 919;  
 Best Local Similarity 100.0%; Pred. No. 0.34;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EYLVPPQGGF 10  
 Db |||||  
 685 EYLVPPQGGF 694  
 Search completed: July 28, 2003, 17:03:42  
 Job time : 83 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run On: July 28, 2003, 17:00:20 ; Search time 96 Seconds  
(without alignments)  
26.880 Million cell updates/sec

Title: US-09-930-125-3  
Perfect score: 54  
Sequence: 1 EYLVPOQGF 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues  
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_23.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phage.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_virus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	367	11 Q8R2X1	Q8R2X1 mus musculus
2	54	100.0	412	4 Q8WYV0	Q8WYV0 homo sapien
3	54	100.0	881	11 Q8C0E7	Q8C0E7 mus musculus
4	54	100.0	1259	6 O18735	O18735 canis famil
5	54	100.0	1259	11 Q8K3P9	Q8K3P9 rattus norv
6	51	94.4	1209	6 Q8M1L8	Q8M1L8 sus scrofa
7	50	92.6	1209	11 Q9QX70	Q9QX70 rattus norv
8	47	87.0	1210	11 Q9EP98	Q9EP98 mus musculus
9	46	85.2	545	15 Q85468	Q85468 avian eryth
10	46	85.2	567	15 Q86714	Q86714 avian rous-
11	46	85.2	729	15 Q86712	Q86712 avian eryth
12	46	85.2	962	15 Q64895	Q64895 avian eryth
13	40	74.1	876	2 Q32739	Q32739 clostridium
14	40	74.1	876	2 Q9KH41	Q9KH41 clostridium
15	38	70.4	910	12 Q9Q9I5	Q9Q9I5 avian adeno
16	37	68.5	75	11 Q88460	Q88460 mus musculus

17	37	68.5	428	16 Q92BW2	Q92BW2 listeria in
18	37	68.5	428	16 Q8Y797	Q8Y797 listeria mo
19	37	68.5	539	3 Q01143	Q01143 magnaporthe
20	37	68.5	694	5 Q9UB16	Q9UB16 caenorhabdi
21	37	68.5	753	5 Q9XZD4	Q9XZD4 caenorhabdi
22	37	68.5	861	5 Q8ML27	Q8ML27 drosophila
23	37	68.5	1137	13 Q9W6F6	Q9W6F6 gallus gall
24	36	66.7	173	2 Q8GLE5	Q8GLE5 xenorhabdus
25	36	66.7	332	4 Q9HAA2	Q9HAA2 homo sapien
26	36	66.7	332	4 Q96CY5	Q96CY5 homo sapien
27	36	66.7	375	4 Q8WVN8	Q8WVN8 homo sapien
28	36	66.7	422	5 Q9VKT8	Q9VKT8 drosophila
29	36	66.7	436	17 Q97Z48	Q97Z48 xenopus lae
30	36	66.7	1730	13 Q8UVY7	Q8UVY7 mus musculu
31	36	66.7	2259	11 Q921C2	Q921C2 mus musculu
32	36	66.7	2304	11 Q921C3	Q921C3 mus musculu
33	36	66.7	3906	2 Q8G987	Q8G987 planktothri
34	35	64.8	209	3 Q94461	Q94461 schizosacch
35	35	64.8	322	16 Q8DD55	Q8DD55 vibrio vuln
36	35	64.8	365	16 Q987M5	Q987M5 rhizobium l
37	35	64.8	481	13 Q8JFP7	Q8JFP7 brachydanio
38	35	64.8	516	3 Q9Y7E1	Q9Y7E1 aspergillus
39	35	64.8	686	11 Q91VG9	Q91VG9 mus musculu
40	35	64.8	686	11 Q9WVJ6	Q9WVJ6 rattus norv
41	35	64.8	686	11 Q8C217	Q8C217 mus musculu
42	35	64.8	852	2 Q9AM64	Q9AM64 acinetobact
43	35	64.8	917	10 Q94C76	Q94C76 arabidopsis
44	35	64.8	1448	5 Q8T683	Q8T683 dictyostell
45	35	64.8	2269	4 Q96QG9	Q96QG9 homo sapien

## ALIGNMENTS

## RESULT 1

Q8R2X1 PRELIMINARY; PRT; 367 AA.  
AC Q8R2X1; Q8R2X1; PRELIMINARY; PRT; 367 AA.  
DT 01-JUN-2002 (TREMBLrel. 21, Created)  
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Hypothetical 40.2 kDa protein.  
OS Mus musculus (Mouse)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Strausberg R.  
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC027080; AAH27080.1; -  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR004019; YLP\_motif.  
DR Pfam; PF00069; pkinase; 1.  
DR Pfam; PF02757; YLP; 2.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
KW Hypothetical protein; ATP-binding; Transferase.  
SQ SEQUENCE 367 AA; 40163 MW; 0BE03395F9E101B0 CRC64;

Query Match 100.0%; Score 54; DB 11; Length 367;  
Best Local Similarity 100.0%; Pred. No. 0.018; Indels 0; Gaps 0;  
Matches: 10; Conservative 0; Mismatches 0;

QY 1 EYLVPOQGF 10  
Db 133 EYLVPOQGF 142

## RESULT 2

Q8WYV0 PRELIMINARY; PRT; 412 AA.  
ID Q8WYV0  
AC Q8WYV0;

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DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN PP3659.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Huang Y., Zhou X.M., Zhang P.P., Jiang H.Q., Qin W.X., Zhao X.T.,
RA Wan D.F., Gu J.R.;
RT "Novel human cDNA clones with function of inhibiting cancer cell
RT growth.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF318349; AAL55856.1; -.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR00719; Prot_kinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR004019; YLP_motif.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF02757; YLP; 2.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00018; EF_HAND; 1.
DR PROSITE; PS00018; EF_HAND; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
KW Hypothetical protein; ATP-binding; Kinase; Transferase;
KW Tyrosine-protein kinase.
SQ SEQUENCE 412 AA; 44702 MW; 034397FF3F27D2BC CRC64;

Query Match 100.0%; Score 54; DB 4; Length 412;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEYLVPOQGF 10
DB 133 EEYLVPOQGF 142

RESULT 3
ID Q8C0E7 PRELIMINARY; PRT; 881 AA.
AC Q8C0E7;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DE 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE V-erb-b2 erythroblastic leukemia viral oncogene homolog 2
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK031542; BAC27442.1; -.
FT NON_TER 1
SQ SEQUENCE 881 AA; 97501 MW; 5D5042BE9F8F0836 CRC64;

Query Match 100.0%; Score 54; DB 11; Length 881;
Best Local Similarity 100.0%; Pred. No. 0.046;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEYLVPOQGF 10
DB 647 EEYLVPOQGF .656

us-09-930-125-3.rspt

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RESULT 4
Q18735 PRELIMINARY; PRT; 1259 AA.
ID Q18735;
AC Q18735;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE ErB-2.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Yokota H.;
RT "cDNA cloning of erbB-2 from canine mammary gland.";
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB008451; BAA23127.1; -.
DR HSP; P11362; IFGK.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000494; EGFR_L_domain.
DR InterPro; IPR006211; Furin-like.
DR InterPro; IPR006212; Furin-repeat.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR004019; YLP_motif.
DR Pfam; PF00757; Furin-like; 1.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF01030; Recep_L_domain; 2.
DR Pfam; PF02757; YLP; 2.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SMC0261; FU; 3.
DR SMART; SMC0219; TyKc; 1.
DR PROSITE; PS00018; EF_HAND; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW ATP-binding; Kinase; Transferase; Tyrosine-protein kinase.
SQ SEQUENCE 1259 AA; 137989 MW; E37364D49C4ACD46 CRC64;

Query Match 100.0%; Score 54; DB 6; Length 1259;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEYLVPOQGF 10
DB 1020 EEYLVPOQGF 1029

RESULT 5
Q8K3F9 PRELIMINARY; PRT; 1259 AA.
ID Q8K3F9;
AC Q8K3F9;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Neu protooncoprotein
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=BDIX;
RA Watson P.A., Kim K., Chen K.-S., Gould M.N.;
RT "Androgen-Dependent Mammary Carcinogenesis in Rats Transgenic for the
RT Neu Proto-Oncogene.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY116182; RAM50093.1; -.
DR InterPro; IPR002048; EF-hand.

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DR InterPro; IPR000494; EGFR_L_domain.
DR InterPro; IPR006211; Furin-like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00757; Furin-like; 1.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF01030; Recep_L_domain; 2.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TK; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00018; EF_HAND; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW ATP-binding; Transferase.
SQ SEQUENCE 1259 AA; 139102 MW; B724BD5CC3AE953 CRC64;

Query Match 100.08; Score 54; DB 11; Length 1259;
Best Local Similarity 100.08; Pred. No. 0.068;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EBYLVPQQGF 10
|||||
Db 1025 EBYLVPQQGF 1034

RESULT 6
Q8MIL8 PRELIMINARY; PRT; 1209 AA.
AC Q8MIL8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Epidermal growth factor receptor.
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim J.G., Vallet J.L., Nonneman D., Christenson R.K.;
RT "Characterization of uterine epidermal growth factor receptor
expression during the estrous cycle and early pregnancy in pigs."
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY117054; AAM77472.1;
DR InterPro; IPR000345; CytC_heme_bind.
DR InterPro; IPR000494; EGFR_L_domain.
DR InterPro; IPR006211; Furin-like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00757; Furin-like; 1.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF01030; Recep_L_domain; 2.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TK; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00190; CYTOCHROME_C; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW ATP-binding; Receptor; Transferase.
SQ SEQUENCE 1209 AA; 133531 MW; 268B3FB11E36F90F CRC64;

Query Match 94.4%; Score 51; DB 6; Length 1209;
Best Local Similarity 90.0%; Pred. No. 0.26;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EBYLVPQQGF 10
|||||
Db 1015 DEYLVPQQGF 1024

RESULT 8
Q9EP98 PRELIMINARY; PRT; 1210 AA.
AC Q9EP98;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Epidermal growth factor receptor isoform 1.
GN EGFR.

Db 1014 DEYLVPQQGF 1023

RESULT 7
Q9QX70 PRELIMINARY; PRT; 1209 AA.
AC Q9QX70;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Epidermal growth factor receptor.
GN EGFR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Fisher; TISSUE=Liver;
RX MEDLINE=90258888; PubMed=2342466;
RA Petch L.A., Harris J., Raymond V.W., Blasband A.J., Lee D.C.,
RA Earp H.S.;
RT "A truncated, secreted form of the epidermal growth factor receptor-is
RT encoded by an alternatively spliced transcript in normal rat tissue.";
RL Mol. Cell. Biol. 10:2973-2982(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Fisher; TISSUE=Liver;
RA Petch L.A.;
RL Submitted (NOV-1991) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Fisher; TISSUE=Liver;
RA Guttridge K., Dawson T.L., Earp H.S.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; M37394; AAF14008.1;
DR HSP; P11362; LFCK.
DR InterPro; IPR000494; EGFR_L_domain.
DR InterPro; IPR006211; Furin-like.
DR InterPro; IPR006212; Furin-repeat.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00757; Furin-like; 1.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF01030; Recep_L_domain; 2.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00261; FU; 3.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW ATP-binding; Kinase; Receptor; Transferase; Tyrosine-protein kinase.
SQ SEQUENCE 1209 AA; 134891 MW; 96FEF7F6CC1B7773 CRC64;

Query Match 92.6%; Score 50; DB 11; Length 1209;
Best Local Similarity 80.0%; Pred. No. 0.41;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EBYLVPQQGF 10
|||||
Db 1015 DEYLVPQQGF 1024

RESULT 8
Q9EP98 PRELIMINARY; PRT; 1210 AA.
AC Q9EP98;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Epidermal growth factor receptor isoform 1.
GN EGFR.

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RP SEQUENCE FROM N.A.
RX MEDLINE=88217326; PubMed=2897102;
RA Scotting P., Vennstrom B., Jansen M., Graf T., Beug H., Haymann M.J.;
OC "Common site of mutation in the erbB gene of avian erythroblastosis
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=C3H/101, 129/SVJ, and 129/SVEV7AC;
RA Reiter J.L., Thredgill D.W., Eley G.D., Strunk K.E., Danielsen A.J.,
RA Sinclair C.S., Pearsall R.S., Green P.J., Yee D., Lampland A.L.,
RA Balasubramanian S., Crossley T.O., Magnuson T.R., James C.D.,
RA Maible N.J.;
RT "Comparative genomic sequence analysis and isolation of human and
RT mouse alternative Egr transcripts encoding truncated receptor
RT isoforms";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Reiter J.L., Thredgill D.W., Eley G.D., Strunk K.E., Danielsen A.J.,
RA Schehl C., Pearsall R.S., Green P.J., Yee D., Lampland A.L.,
RA Balasubramanian S., Crossley T.O., Magnuson T.R., James C.D.,
RA Maible N.J.;
RT "Comparative genomic sequence analysis and isolation of human and
RT mouse alternative Egr transcripts encoding truncated receptor
RT isoforms";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF275366; AAG28045.1; -.
DR EMBL; AF275364; AAG28045.1; JOINED.
DR EMBL; AF275365; AAG28045.1; JOINED.
DR EMBL; AF275367; AAG24386.1; -.
DR HSP; P11362; IFCK.
DR MGD; MGI:95294; Egr.
DR InterPro; IPR000345; CytC_heme_bind.
DR InterPro; IPR000494; EGFR_L_domain.
DR InterPro; IPR006211; Furin-like.
DR InterPro; IPR006212; Furin-repeat.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00757; Furin-like; 1.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF01030; Recep_L_domain; 2.
DR PRINTS; PR00109; TYRKINASE.
DR PRODOM; PD000001; Prot_kinase; 1.
DR SMART; SM00261; FU; 3.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00190; CYTOCHROME_C; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00109; Tyrosine-protein kinase.
DR ATP-binding; Kinase; Receptor; Transferase; Tyrosine-protein kinase.
DR KW SEQUENCE 1210 AA; 134840 MW; 62CD021C9DE32E18 CRC64;
SQ SEQUENCE 1210 AA; 134840 MW; 62CD021C9DE32E18 CRC64;
Query Match 87.0%; Score 47; DB 11; Length 1210;
Best Local Similarity 80.0%; Pred. No. 1.6;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 EYLVPOQGF 10
DB 1016 DEYLVPOQGF 1025
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Reiter J.L., Thredgill D.W., Eley G.D., Strunk K.E., Danielsen A.J.,
RA Schehl C., Pearsall R.S., Green P.J., Yee D., Lampland A.L.,
RA Balasubramanian S., Crossley T.O., Magnuson T.R., James C.D.,
RA Maible N.J.;
RT "Comparative genomic sequence analysis and isolation of human and
RT mouse alternative Egr transcripts encoding truncated receptor
RT isoforms";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF275366; AAG28045.1; -.
DR EMBL; AF275364; AAG28045.1; JOINED.
DR EMBL; AF275365; AAG28045.1; JOINED.
DR EMBL; AF275367; AAG24386.1; -.
DR HSP; P11362; IFCK.
DR MGD; MGI:95294; Egr.
DR InterPro; IPR000345; CytC_heme_bind.
DR InterPro; IPR000494; EGFR_L_domain.
DR InterPro; IPR006211; Furin-like.
DR InterPro; IPR006212; Furin-repeat.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00757; Furin-like; 1.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF01030; Recep_L_domain; 2.
DR PRINTS; PR00109; TYRKINASE.
DR PRODOM; PD000001; Prot_kinase; 1.
DR SMART; SM00261; FU; 3.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00190; CYTOCHROME_C; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00109; Tyrosine-protein kinase.
DR ATP-binding; Kinase; Receptor; Transferase; Tyrosine-protein kinase.
DR KW SEQUENCE 1210 AA; 134840 MW; 62CD021C9DE32E18 CRC64;
SQ SEQUENCE 1210 AA; 134840 MW; 62CD021C9DE32E18 CRC64;
Query Match 87.0%; Score 47; DB 11; Length 1210;
Best Local Similarity 80.0%; Pred. No. 1.6;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 EYLVPOQGF 10
DB 1016 DEYLVPOQGF 1025
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Reiter J.L., Thredgill D.W., Eley G.D., Strunk K.E., Danielsen A.J.,
RA Schehl C., Pearsall R.S., Green P.J., Yee D., Lampland A.L.,
RA Balasubramanian S., Crossley T.O., Magnuson T.R., James C.D.,
RA Maible N.J.;
RT "Comparative genomic sequence analysis and isolation of human and
RT mouse alternative Egr transcripts encoding truncated receptor
RT isoforms";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF275366; AAG28045.1; -.
DR EMBL; AF275364; AAG28045.1; JOINED.
DR EMBL; AF275365; AAG28045.1; JOINED.
DR EMBL; AF275367; AAG24386.1; -.
DR HSP; P11362; IFCK.
DR MGD; MGI:95294; Egr.
DR InterPro; IPR000345; CytC_heme_bind.
DR InterPro; IPR000494; EGFR_L_domain.
DR InterPro; IPR006211; Furin-like.
DR InterPro; IPR006212; Furin-repeat.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00757; Furin-like; 1.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF01030; Recep_L_domain; 2.
DR PRINTS; PR00109; TYRKINASE.
DR PRODOM; PD000001; Prot_kinase; 1.
DR SMART; SM00261; FU; 3.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00190; CYTOCHROME_C; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00109; Tyrosine-protein kinase.
DR ATP-binding; Kinase; Receptor; Transferase; Tyrosine-protein kinase.
DR KW SEQUENCE 1210 AA; 134840 MW; 62CD021C9DE32E18 CRC64;
SQ SEQUENCE 1210 AA; 134840 MW; 62CD021C9DE32E18 CRC64;
Query Match 87.0%; Score 47; DB 11; Length 1210;
Best Local Similarity 80.0%; Pred. No. 1.6;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 EYLVPOQGF 10
DB 1016 DEYLVPOQGF 1025
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Reiter J.L., Thredgill D.W., Eley G.D., Strunk K.E., Danielsen A.J.,
RA Schehl C., Pearsall R.S., Green P.J., Yee D., Lampland A.L.,
RA Balasubramanian S., Crossley T.O., Magnuson T.R., James C.D.,
RA Maible N.J.;
RT "Comparative genomic sequence analysis and isolation of human and
RT mouse alternative Egr transcripts encoding truncated receptor
RT isoforms";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF275366; AAG28045.1; -.
DR EMBL; AF275364; AAG28045.1; JOINED.
DR EMBL; AF275365; AAG28045.1; JOINED.
DR EMBL; AF275367; AAG24386.1; -.
DR HSP; P11362; IFCK.
DR MGD; MGI:95294; Egr.
DR InterPro; IPR000345; CytC_heme_bind.
DR InterPro; IPR000494; EGFR_L_domain.
DR InterPro; IPR006211; Furin-like.
DR InterPro; IPR006212; Furin-repeat.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00757; Furin-like; 1.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF01030; Recep_L_domain; 2.
DR PRINTS; PR00109; TYRKINASE.
DR PRODOM; PD000001; Prot_kinase; 1.
DR SMART; SM00261; FU; 3.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00190; CYTOCHROME_C; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00109; Tyrosine-protein kinase.
DR ATP-binding; Kinase; Receptor; Transferase; Tyrosine-protein kinase.
DR KW SEQUENCE 1210 AA; 134840 MW; 62CD021C9DE32E18 CRC64;
SQ SEQUENCE 1210 AA; 134840 MW; 62CD021C9DE32E18 CRC64;
Query Match 87.0%; Score 47; DB 11; Length 1210;
Best Local Similarity 80.0%; Pred. No. 1.6;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 EYLVPOQGF 10
DB 1016 DEYLVPOQGF 1025
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Reiter J.L., Thredgill D.W., Eley G.D., Strunk K.E., Danielsen A.J.,
RA Schehl C., Pearsall R.S., Green P.J., Yee D., Lampland A.L.,
RA Balasubramanian S., Crossley T.O., Magnuson T.R., James C.D.,
RA Maible N.J.;
RT "Comparative genomic sequence analysis and isolation of human and
RT mouse alternative Egr transcripts encoding truncated receptor
RT isoforms";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF275366; AAG28045.1; -.
DR EMBL; AF275364; AAG28045.1; JOINED.
DR EMBL; AF275365; AAG28045.1; JOINED.
DR EMBL; AF275367; AAG24386.1; -.
DR HSP; P11362; IFCK.
DR MGD; MGI:95294; Egr.
DR InterPro; IPR000345; CytC_heme_bind.
DR InterPro; IPR000494; EGFR_L_domain.
DR InterPro; IPR006211; Furin-like.
DR InterPro; IPR006212; Furin-repeat.

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RESULT 11
Q06712          PRELIMINARY;          PRT;    729 AA.
ID  Q06712
AC  Q06712;
DT  01-NOV-1996 (TREMblrel. 01, Created)
DT  01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT  01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE  Polyprotein.
GN  POLYPROTEIN.
OS  Avian rous-associated virus type 1.
OC  Viruses; Retroviral viruses; Retroviridae; Alpharetrovirus.
OX  NCBI_TaxID=11950;
RN  [1]
RP  MEDLINE=94203659; PubMed=8152791;
RX  Vennstrom B., Raynoscheck C., Jansson L., Doederlein G., Lhotak V.,
RA  Johnson A., Beug H.;
RT  "Retroviral capture of c-erbB proto-oncogene sequences: rapid
RT  evolution of distinct viral genomes carrying mutant v-erbB genes with
RT  different transforming capacities.";
RL  Oncogene 9:1307-1320(1994).
DR  EMBL; S89372; AAC60725.1; -.
DR  HSSP; P03322; 1A6S.
DR  InterPro; IPR000719; Prot_kinase.
DR  InterPro; IPR004028; Retro_M.
DR  InterPro; IPR001245; Tyr_kinase.
DR  Pfam; PF00069; pkinase; 1.
DR  Pfam; PF02813; Retro_M; 1.
DR  PRINTS; PR00109; TYRKINASE.
DR  ProDom; PD000001; Prot_kinase; 1.
DR  SMART; SM00219; TYRK; 1.
DR  PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR  PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR  PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW  ATP-binding; Kinase; Tyrosine-protein kinase.
SQ  SEQUENCE 729 AA; 80649 MW; 84D2F6914EFE1D63 CRC64;

Query Match      85.2%; Score 46; DB 15; Length 729;
Best Local Similarity 80.0%; Pred. No. 1.5;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy  1 EYLVPOQGF 10
Db  588 DEYLVPHQGF 597

RESULT 12
Q064895          PRELIMINARY;          PRT;    962 AA.
ID  Q064895
AC  Q064895;
DT  01-NOV-1996 (TREMblrel. 01, Created)
DT  01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT  01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE  Gag, v-erb-A, v-erb-B protein.
DR  EMBL; X52211; CAA36459.1; -.
DR  HSSP; P10828; 2NLL.
OS  Avian erythroblastosis virus.
OC  Viruses; Retroviral viruses; Retroviridae; Avian type C retroviruses.
OX  NCBI_TaxID=11861;
RN  [1]
RP  MEDLINE=90206603; PubMed=1969616;
RX  Bruskun A., Jackson J., Bishop J.M., McCarley D.J., Schatzman R.C.;
RA  "Six amino acids from the retroviral gene gag greatly enhance the
RT  transforming potential of the oncogene v-erb-B.";
RL  Oncogene 5:15-24(1990).
CC  -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC  -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
DR  EMBL; X52209; CAA36459.1; -.
DR  EMBL; X52211; CAA36459.1; JOINED.
DR  HSSP; P10828; 2NLL.
DR  InterPro; IPR000536; Hormone_rec_lig.
DR  InterPro; IPR000719; Prot_kinase.

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DR  InterPro; IPR001723; Stdhrmn_receptor.
DR  InterPro; IPR001245; Tyr_kinase.
DR  InterPro; IPR001628; Znf_C4steroid.
DR  Pfam; PF00104; hormone_rec; 1.
DR  Pfam; PF00069; pkinase; 1.
DR  Pfam; PF00105; zf-C4; 1.
DR  PRINTS; PR00398; STRDHORMONER.
DR  PRINTS; PR00047; STROIDFINGER.
DR  PRINTS; PR00109; TYRKINASE.
DR  ProDom; PD000001; Prot_kinase; 1.
DR  ProDom; PD000035; Znf_C4steroid; 1.
DR  SMART; SM00430; HOLI; 1.
DR  SMART; SM00219; TYRK; 1.
DR  SMART; SM00399; ZNF_C4; 1.
DR  PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
DR  PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR  PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR  PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW  ATP-binding; DNA-binding; Kinase; Metal-binding; Nuclear protein;
KW  Receptor; Transcription; Transcription regulation; Transferase;
KW  Tyrosine-protein kinase; Zinc; Zinc-finger.
SQ  SEQUENCE 962 AA; 108320 MW; 3C5AED791E4E95CE CRC64;

Query Match      85.2%; Score 46; DB 15; Length 962;
Best Local Similarity 80.0%; Pred. No. 2;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy  1 EYLVPOQGF 10
Db  856 DEYLVPHQGF 865

RESULT 13
Q032739          PRELIMINARY;          PRT;    876 AA.
ID  Q032739
AC  Q032739;
DT  01-JAN-1998 (TREMblrel. 05, Created)
DT  01-JAN-1998 (TREMblrel. 05, Last sequence update)
DT  01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE  ADP-ribosyltransferase.
GN  CDTB.
OS  Clostridium difficile.
OC  Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC  Clostridium.
OX  NCBI_TaxID=1496;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=CD196;
RX  MEDLINE=97230316; PubMed=9119480;
RA  Perelle S., Gibert M., Bourlioux P., Corthier G., Popoff M.R.;
RT  "Production of a complete binary toxin (actin-specific ADP-
RT  ribosyltransferase) by Clostridium difficile CDI96.";
RL  Infect. Immun. 65:1402-1407(1997).
DR  EMBL; L76081; AAB67305.1; -.
DR  HSSP; P13423; 1ACC.
DR  InterPro; IPR003896; Anthrax_toxinB.
DR  Pfam; PF03495; Binary_toxB; 1.
DR  PRINTS; PR01391; BINARYTOXINB.
KW  Transferase.
SQ  SEQUENCE 876 AA; 98797 MW; 25E06E2D45CE2B3B CRC64;

Query Match      74.1%; Score 40; DB 2; Length 876;
Best Local Similarity 66.7%; Pred. No. 30;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy  2 EYLVPOQGF 10
Db  696 DYLVPEQGY 704

RESULT 14
Q9KH41          PRELIMINARY;          PRT;    876 AA.
ID  Q9KH41

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AC Q9KH41;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE CdtB.  
 GN CdtB.  
 OS Clostridium difficile.  
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 OC Clostridium.  
 OX NCBI\_TaxID=1496;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CCUG 20309;  
 RA Chang S.Y., Song K.P.;  
 RT "ADP-ribosylating Binary Toxin Genes of Clostridium difficile strain  
 RT CCUG 20309";  
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF271719; AAF81761.1; -;  
 DR HSSP; P13423; LACC.  
 DR InterPro; IPR003896; Anthrax toxinB.  
 DR Pfam; PF03495; Binary toxinB.1.  
 DR PRINTS; PR01391; BINARYTOXINB.  
 SQ SEQUENCE 876 AA; 98793 MW; 366D62F352E745A5 CRC64;

Query Match 74.1%; Score 40; DB 2; Length 876;  
 Best Local Similarity 66.7%; Pred. No. 30;  
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 EYLVPOQGF 10  
 :|:|:|:|:  
 Db 696 DYLVPEQGY 704

RESULT 15  
 Q90915  
 ID Q90915 PRELIMINARY; PRT; 910 AA.  
 AC Q90915;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE 100 kDa protein homolog (Fragment).  
 OS Avian adenovirus type 8 (strain ATCC A-2A) (Fowl adenovirus 8).  
 OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Aviadenovirus.  
 OX NCBI\_TaxID=66295;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CFA40;  
 RA Johnson M.A., Pooley C.;  
 RL "Fowl adenovirus serotype 8 hypervirulent strain CFA40.";  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF155911; AAF17336.1; -;  
 DR InterPro; IPR003381; Adeno\_100.  
 DR Pfam; PF02438; adeno\_100; 1.  
 FT NON\_TER 1  
 SQ SEQUENCE 910 AA; 102772 MW; EB0BA4227ED2CEC CRC64;

Query Match 70.4%; Score 38; DB 12; Length 910;  
 Best Local Similarity 66.7%; Pred. No. 78;  
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEYLVPOQG 9  
 ||:|:|:|:  
 Db 855 EEFLPEQG 863

Search completed: July 28, 2003, 17:05:58  
 Job time : 100 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 28, 2003, 17:02:20 ; Search time 29 Seconds  
(without alignments)  
14,590 Million cell updates/sec

Title: US-09-930-125-3  
Perfect score: 54  
Sequence: 1 EYLVPPQGGF 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	580	1	US-08-414-417B-69
2	54	100.0	580	2	US-08-486-348A-69
3	54	100.0	580	2	US-08-468-545B-69
4	54	100.0	580	3	US-08-466-680B-69
5	54	100.0	1255	1	US-08-467-083-68
6	54	100.0	1255	1	US-08-414-417B-68
7	54	100.0	1255	2	US-08-484-438-8
8	54	100.0	1255	2	US-08-486-348A-68
9	54	100.0	1255	2	US-08-625-101-2
10	54	100.0	1255	2	US-08-468-545B-68
11	54	100.0	1255	2	US-08-356-786-2
12	54	100.0	1255	3	US-08-466-680B-68
13	54	100.0	1255	4	US-09-527-487-2
14	50	92.6	13	1	US-08-128-971B-12
15	50	92.6	1210	2	US-08-484-438-7
16	50	92.6	1210	2	US-08-475-035-4
17	42	77.8	13	1	US-08-408-604A-69
18	37	68.5	512	3	US-09-356-818A-2
19	37	68.5	541	2	US-08-484-438-6
20	37	68.5	548	1	US-08-247-902A-2
21	37	68.5	548	5	PCT-US93-10541-2
22	37	68.5	687	5	PCT-US91-09784-2
23	37	68.5	705	2	US-08-456-647B-4
24	37	68.5	705	2	US-08-237-401A-4
25	37	68.5	1058	2	US-08-484-438-4
26	37	68.5	1308	2	US-08-484-438-2
27	36	66.7	9	5	PCT-US93-01669-56

28	36	66.7	209	4	US-09-252-991A-30648	Sequence 30648, A
29	35	64.8	516	4	US-09-215-694-16	Sequence 16, Appl
30	35	64.8	685	5	PCT-US91-09784-4	Sequence 4, Appl
31	34	63.0	182	4	US-09-328-352-8193	Sequence 8193, Ap
32	34	63.0	590	4	US-09-252-991A-19046	Sequence 19046, A
33	33	61.1	9	1	US-08-178-570-63	Sequence 63, Appl
34	33	61.1	9	3	US-08-369-643-63	Sequence 63, Appl
35	33	61.1	9	5	PCT-US95-00147-63	Sequence 63, Appl
36	33	61.1	12	1	US-08-406-192-1	Sequence 1, Appl
37	33	61.1	12	2	US-08-545-151-1	Sequence 1, Appl
38	33	61.1	12	6	5169933-12	Patent No. 5169933
39	33	61.1	27	6	5169933-43	Patent No. 5169933
40	33	61.1	371	4	US-09-252-991A-27127	Sequence 27127, A
41	33	61.1	442	2	US-08-821-355A-5	Sequence 5, Appl
42	33	61.1	442	2	US-09-003-687A-5	Sequence 5, Appl
43	33	61.1	442	3	US-09-136-605-5	Sequence 5, Appl
44	33	61.1	491	4	US-09-252-991A-29041	Sequence 29041, A
45	33	61.1	581	2	US-08-724-394A-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1  
US-08-414-417B-69  
; Sequence 69, Application US/08414417B  
; Patent No. 5801005  
; GENERAL INFORMATION:  
; APPLICANT: Cheever, Martin A.  
; APPLICANT: Disis, Mary L.  
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH  
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/414,417B  
; FILING DATE: 31-MAR-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sharkey, Richard G.  
; REGISTRATION NUMBER: 32,629  
; REFERENCE/DOCKET NUMBER: 920010.448C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 69:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 580 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
US-08-414-417B-69

Query Match 100.0%; Score 54; DB 1; Length 580;  
Best Local Similarity 100.0%; Pred. No. 0.029;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EYLVPPQGGF 10  
DB 346 EYLVPPQGGF 355

RESULT 2

US-08-486-348A-69  
Sequence 69, Application US/08486348A  
Patent No. 5846538

GENERAL INFORMATION:

APPLICANT: Cheever, Martin A.

APPLICANT: Disis, Mary L.

TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN

TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE

TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED

NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed and Berry LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: US

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/486,348A

FILING DATE: 07-JUN-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Sharkey, Richard G.

REGISTRATION NUMBER: 32,629

REFERENCE/DOCKET NUMBER: 920010.448C6

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 69:

SEQUENCE CHARACTERISTICS:

LENGTH: 580 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

US-08-486-348A-69

Query Match 100.0%; Score 54; DB 2; Length 580;

Best Local Similarity 100.0%; Pred. No. 0.029;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EYLVPQGF 10

Db 346 EYLVPQGF 355

RESULT 3

US-08-486-545B-69  
Sequence 69, Application US/08468545B  
Patent No. 5876712

GENERAL INFORMATION:

APPLICANT: Cheever, Martin A.

APPLICANT: Disis, Mary L.

TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN

TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE

TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED

NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed and Berry LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: US

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

Query Match 100.0%; Score 54; DB 3; Length 580;

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/468,545B

FILING DATE: 06-JUN-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Sharkey, Richard G.

REGISTRATION NUMBER: 32,629

REFERENCE/DOCKET NUMBER: 920010.448C5

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 69:

SEQUENCE CHARACTERISTICS:

LENGTH: 580 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

US-08-468-545B-69

Query Match 100.0%; Score 54; DB 2; Length 580;

Best Local Similarity 100.0%; Pred. No. 0.029;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EYLVPQGF 10

Db 346 EYLVPQGF 355

RESULT 4

US-08-466-680B-69

Sequence 69, Application US/08466680B

Patent No. 6075122

GENERAL INFORMATION:

APPLICANT: Cheever, Martin A.

APPLICANT: Disis, Mary L.

TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN

TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE

TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED

NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed and Berry LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: US

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/466,680B

FILING DATE: 06-JUN-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Sharkey, Richard G.

REGISTRATION NUMBER: 32,629

REFERENCE/DOCKET NUMBER: 920010.448C4

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 69:

SEQUENCE CHARACTERISTICS:

LENGTH: 580 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

US-08-466-680B-69

Query Match

100.0%; Score 54; DB 3; Length 580;

6075122

DP for Sure 13267

Best Local Similarity 100.0%; Pred. No. 0.029;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EYLVPQOGF 10  
Db 346 EYLVPQOGF 355

RESULT 5  
US-08-467-083-68  
; Sequence 68, Application US/08467083  
; Patent No. 5726023  
; GENERAL INFORMATION:  
; APPLICANT: Cheever, Martin A.  
; APPLICANT: Disis, Mary L.  
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN  
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
; TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED  
; NUMBER OF SEQUENCES: 68  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/414,417  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 424  
; PRIORITY INFORMATION:  
; PRIORITY APPLICATION NUMBER: US 08/414,417  
; FILING DATE: 06-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sharkey, Richard G.  
; REGISTRATION NUMBER: 32,629  
; REFERENCE/DOCKET NUMBER: 920010.448C2  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; TELEX: 3723836 SEEDANBERRY  
; INFORMATION FOR SEQ ID NO: 68:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1255 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-08-467-083-68

Query Match 100.0%; Score 54; DB 1; Length 1255;  
Best Local Similarity 100.0%; Pred. No. 0.066;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EYLVPQOGF 10  
Db 1021 EYLVPQOGF 1030

RESULT 6  
US-08-414-417B-68  
; Sequence 68, Application US/08414417B  
; Patent No. 5801005  
; GENERAL INFORMATION:  
; APPLICANT: Cheever, Martin A.  
; APPLICANT: Disis, Mary L.  
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN  
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
; TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED  
; NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/414,417B  
FILING DATE: 31-MAR-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharkey, Richard G.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C2  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 68:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1255 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-414-417B-68

Query Match 100.0%; Score 54; DB 1; Length 1255;  
Best Local Similarity 100.0%; Pred. No. 0.066;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EYLVPQOGF 10  
Db 1021 EYLVPQOGF 1030

RESULT 7  
US-08-484-438-8  
; Sequence 8, Application US/08484438  
; Patent No. 5811098  
; Patent No. 5811098 5780031  
; GENERAL INFORMATION:  
; APPLICANT: Plowman, Gregory D.  
; APPLICANT: Culouscou, Jean-Michel  
; APPLICANT: Shoyab, Mohammed  
; APPLICANT: Siegall, Clay B.  
; APPLICANT: Hellstr m, Ingegerd  
; APPLICANT: Hellstr m, Karl E.  
; TITLE OF INVENTION: HER4 HUMAN RECEPTOR TYROSINE KINASE  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,438  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 530  
PRIORITY INFORMATION:  
PRIORITY APPLICATION NUMBER: 08/323,442  
FILING DATE: 14-OCT-1994  
APPLICATION NUMBER: US 08/150,704

FILING DATE: 10-NOV-1993  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/981,165  
FILING DATE: 24-NOV-1992  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Misrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 5624-230  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 990-9090  
TELEFAX: (212) 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1255 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-486-438-8

Query Match 100.0%; Score 54; DB 2; Length 1255;  
Best Local Similarity 100.0%; Pred. No. 0.066;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EYLVPOQGF 10  
Db 1021 EYLVPOQGF 1030

RESULT 8  
US-08-486-348A-68  
; Sequence 68, Application US/08486348A  
; Patent No. 5846538  
; GENERAL INFORMATION:  
; APPLICANT: Cheever, Martin A.  
; APPLICANT: Disis, Mary L.  
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0; Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/486/348A  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sharkey, Richard G.  
; REGISTRATION NUMBER: 32,629  
; REFERENCE/DOCKET NUMBER: 920010.448C6  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 68:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1255 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-08-486-348A-68

DP on

Query Match 100.0%; Score 54; DB 2; Length 1255;  
Best Local Similarity 100.0%; Pred. No. 0.066;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EYLVPOQGF 10  
Db 1021 EYLVPOQGF 1030

RESULT 9  
US-08-625-101-2  
; Sequence 2, Application US/08625101  
; Patent No. 5869445  
; GENERAL INFORMATION:  
; APPLICANT: Cheever, Martin A.  
; APPLICANT: Disis, Mary L.  
; TITLE OF INVENTION: COMPOUNDS FOR ELICITING OR ENHANCING IMMUNE  
; TITLE OF INVENTION: REACTIVITY TO HER-2/neu PROTEIN FOR PREVENTION  
; TITLE OF INVENTION: OR TREATMENT OF MALIGNANCIES IN WHICH THE HER-2/neu  
; TITLE OF INVENTION: ONCOGENE IS ASSOCIATED  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0; Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/625/101  
; FILING DATE: 01-APR-1996  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sharkey, Richard G.  
; REGISTRATION NUMBER: 32,629  
; REFERENCE/DOCKET NUMBER: 920010.448C7  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1255 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-625-101-2

5869445

DP for gene?

Query Match 100.0%; Score 54; DB 2; Length 1255;  
Best Local Similarity 100.0%; Pred. No. 0.066;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EYLVPOQGF 10  
Db 1021 EYLVPOQGF 1030

RESULT 10  
US-08-468-545B-68  
; Sequence 68, Application US/08468545B  
; Patent No. 5876712  
; GENERAL INFORMATION:  
; APPLICANT: Cheever, Martin A.  
; APPLICANT: Disis, Mary L.  
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:

DP

ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/468,545B  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharkey, Richard G.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 68:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1255 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-468-545B-68

Query Match 100.0%; Score 54; DB 2; Length 1255;  
Best Local Similarity 100.0%; Pred. No. 0.066;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EYLVPOQGF 10  
Db 1021 EYLVPOQGF 1030

RESULT 11  
US-08-356-786-2

Sequence 2, Application US/08356786  
Patent No. 5877305

GENERAL INFORMATION:  
APPLICANT: Huston, James S.  
APPLICANT: Oppermann, Hermann  
APPLICANT: Houston, L. L.  
APPLICANT: Ring, David B.  
TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibault  
STREET: Exchange Place, 53 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/356,786  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/831,967  
FILING DATE: 06-FEB-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Pitcher, Edmund R.  
REGISTRATION NUMBER: 27,829  
REFERENCE/DOCKET NUMBER: CRP-053

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 248-7000  
TELEFAX: (617) 248-7100  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1255 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-356-786-2

Query Match 100.0%; Score 54; DB 2; Length 1255;  
Best Local Similarity 100.0%; Pred. No. 0.066;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EYLVPOQGF 10  
Db 1021 EYLVPOQGF 1030

RESULT 12

US-08-466-680B-68

Sequence 68, Application US/08466680B  
Patent No. 6075122

GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.

APPLICANT: Disis, Mary L.

TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN

TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED

NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed and Berry LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: US

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/466,680B

FILING DATE: 06-JUN-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Sharkey, Richard G.

REGISTRATION NUMBER: 32,629

REFERENCE/DOCKET NUMBER: 920010.448C4

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 68:

SEQUENCE CHARACTERISTICS:

LENGTH: 1255 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-466-680B-68

Query Match 100.0%; Score 54; DB 3; Length 1255;  
Best Local Similarity 100.0%; Pred. No. 0.066;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EYLVPOQGF 10  
Db 1021 EYLVPOQGF 1030

RESULT 13

US-09-527-487-2

Sequence 2, Application US/09527487



; Patent No. 6528060  
; GENERAL INFORMATION:  
; APPLICANT: Nicolette, Charles  
; TITLE OF INVENTION: HER2 ANTIGENIC PEPTIDES  
; FILE REFERENCE: 126881309200  
; CURRENT APPLICATION NUMBER: US/09/527,487  
; CURRENT FILING DATE: 2000-03-16  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 1255  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-527-487-2

Query Match 100.0%; Score 54; DB 4; Length 1255;  
Best Local Similarity 100.0%; Pred. No. 0.066; 0; Indels 0; Gaps 0;  
Matches 10; Conservative 0; Mismatches 0;

QY 1 EYLVPPQGF 10  
1021 EYLVPPQGF 1030

RESULT 14  
US-08-128-971B-12  
; Sequence 12, Application US/08128971B  
; Patent No. 5525503  
; GENERAL INFORMATION:  
; APPLICANT: Christopher E. Rudd  
; APPLICANT: Prasad Kanteti  
; TITLE OF INVENTION: SIGNAL TRANSDUCTION VIA CD28  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; COMPUTER: IBM PS/2 Model 502 or 55Sx  
; OPERATING SYSTEM: MS-DOS (Version 5.0)  
; SOFTWARE: WordPerfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/128,971B  
; FILING DATE: September 28, 1993  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:

; ATTORNEY/AGENT INFORMATION:  
; NAME: Janis K. Fraser  
; REGISTRATION NUMBER: 34,919  
; REFERENCE/DOCKET NUMBER: 00530/073001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 542-5070  
; TELEFAX: (617) 542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 13  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
US-08-128-971B-12

Query Match 92.6%; Score 50; DB 1; Length 13;  
Best Local Similarity 80.0%; Pred. No. 0.0027; 0; Indels 0; Gaps 0;  
Matches 8; Conservative 2; Mismatches 0;

QY 1 EYLVPPQGF 10

Db 3 DEYLIPOQGF 12  
:|||||

RESULT 15  
US-08-484-438-7  
; Sequence 7, Application US/08484438  
; Patent No. 5811098  
; Patent No. 5811098 5780031  
; GENERAL INFORMATION:  
; APPLICANT: Plowman, Gregory D.  
; APPLICANT: Culouscou, Jean-Michel  
; APPLICANT: Shoyab, Mohammed  
; APPLICANT: Siegall, Clay B.  
; APPLICANT: Hellstr m, Ingegerd  
; APPLICANT: Hellstr m, Karl E.  
; TITLE OF INVENTION: HER4 HUMAN RECEPTOR TYROSINE KINASE  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/484,438  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/323,442  
; FILING DATE: 14-OCT-1994  
; APPLICATION NUMBER: US 08/150,704  
; FILING DATE: 10-NOV-1993  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/981,165  
; FILING DATE: 24-NOV-1992  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 5624-230  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-8864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1210 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
US-08-484-438-7

Query Match 92.6%; Score 50; DB 2; Length 1210;  
Best Local Similarity 80.0%; Pred. No. 0.36;  
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EYLVPPQGF 10  
1014 DEYLIPOQGF 1023  
:|||||

Search completed: July 28, 2003, 17:07:18  
Job time : 30 secs